

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 ; Search time 20.18 Seconds

(without alignments)  
1102.527 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953

Sequence: 1 MKSKVLALLPALLAAGAAH.....TRDAGINTNIVAGLVYQF 367

Scoring table: BLOSUM62

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseqp/AA1983.DAT.\*  
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8: /SID88/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
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12: /SID88/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
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16: /SID88/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	20	AAV42549
2	1914	98.0	367	20	AAV34058
3	1914	98.0	367	21	AAV57356
4	1285	65.8	377	20	AAV34057
5	1285	65.8	377	21	AAV57355
6	1104	56.5	362	20	AAV42550
7	1078.5	55.2	323	20	AAV34056
8	1078.5	55.2	323	21	AAV57354
9	1027	52.6	340	17	AAW92998
10	226.5	11.6	89	18	AAW27781
11	187.5	9.6	353	20	AAV26025

12	176	9.0	362	10	AAV90098	P2 antigen of Haem
13	174	8.9	353	20	AAV26024	OMP protein of Pa
14	171	8.8	343	20	AAV26023	OMP protein of Pa
15	164.5	8.4	361	11	AAV05999	P2 gene product of
16	164.5	8.4	361	16	AAV66877	H. influenzae P2 e
17	161.5	8.3	390	18	AAW21678	Haemophilus influe
18	148.5	7.6	350	13	AAW27484	Protein IB. Synth
19	147.5	7.5	353	11	AAV90100	Class II outer mem
20	146	7.5	352	16	AAV69607	Gonococcal porin-5
21	145.5	7.5	372	16	AAV69607	Mature class 2 por
22	140.5	7.2	342	16	AAV70763	Neisseria meningit
23	140.5	7.2	342	18	AAW21742	Fusion Class 2 por
24	140.5	7.2	363	16	AAV70764	Neisseria meningit
25	140.5	7.2	363	18	AAW21743	Class IB outer mem
26	132	6.8	328	11	AAV60366	P3 gene product of
27	130.5	6.7	341	11	AAV07043	A surface protein
28	128.5	6.6	589	20	AAV23745	Class IA outer mem
29	127.5	6.5	326	11	AAV6037	PNV-2 fusion const
30	127.5	6.5	363	16	AAV66878	Class I OMP derive
31	127.5	6.5	373	11	AAV6043	H. influenzae prot
32	126.5	6.5	342	16	AAV66879	Class I OMP derive
33	126.5	6.5	342	16	AAV66880	Meningococcal p1.7
34	126.5	6.5	366	11	AAV6044	Class I OMP derive
35	125.5	6.4	373	14	AAV3728	Class I OMP derive
36	125	6.4	368	11	AAV06042	Class I OMP derive
37	124.5	6.4	341	11	AAV07042	P3 gene product of
38	124.5	6.4	511	17	AAV95012	C. difficile toxin
39	124.5	6.4	511	17	AAV5371	C. difficile toxin
40	124.5	6.4	608	17	AAV95013	C. difficile toxin
41	124.5	6.4	609	17	AAV95018	C. difficile toxin
42	124.5	6.4	611	17	AAV5372	C. difficile toxin
43	124.5	6.4	2366	17	AAV5011	C. difficile toxin
44	124.5	6.4	2366	19	AAV68388	Clostridium diffic
45	121	6.2	373	11	AAV6035	Class I outer memb

#### ALIGNMENTS

RESULT 1	AAV42549	standard; Protein: 367 AA.
AC	AAV42549:	
XX		
DT	20-DEC-1999	(first entry)
XX		
DE	E. coli wild-type ompc protein.	
XX		
KW	Bacteria; attenuation; deletion; mutant; vaccine; immune response;	
KW	Gram negative; infection; diarrhoea; food poisoning; typhoid;	
KW	salmonellosis; gonorrhoea; gastroenteritis; whooping cough.	
XX		
OS	Escherichia coli.	
XX		
PN	WO949026-A1.	
XX		
PD	30-SEP-1999.	
XX		
PE	25-MAR-1999;	99WO-GB00935.
XX		
PR	25-MAR-1998;	98GB-0006449.
XX		
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.	
XX		
PI	Chatfield SN;	
XX		
DR	WPI: 1999-580447/49.	
XX		
DR	N-PSDB; AA222885.	
XX		
PT	New attenuated bacteria useful as vaccines for protecting against	
XX	infections	

Disclosure; Page 57-58; 69pp; English.

xx Disclosure; Page 57-58; 69pp; English.

cc This sequence represents the *E. coli* wild-type ompC protein. The coding  
cc sequence of the ompC gene was removed via PCR using primers TT7-rr10  
cc (AAZ22893-722896) to produce a non-reverting deletion mutation. The  
cc mutant ompC gene (AAZ22886) was used in the production of a bacterium  
cc attenuated by a non-reverting mutation in each of the ompC gene, the *aroC*  
cc gene (AAZ22883, AAZ22884), and the ompF gene (AAZ22887, AAZ22888). The  
cc mutant bacteria provide immunogenic activity with reduced virulence and  
cc thus can be used as a vaccine for raising an immune response against a  
cc variety of bacteria in a mammalian host. Such vaccines can provide  
cc protection against e.g., *E. coli* (a cause of diarrhoea in humans),  
cc *Salmonella typhimurium* (the cause of salmonellosis in several animal  
cc species), *S. typhi* (the cause of human typhoid), *S. enteritidis* (a cause  
cc of food poisoning in humans), *S. choleraesuis* (a cause of salmonellosis  
cc in pigs), *S. dublin* (a cause of both a systemic and diarrhoeal disease in  
cc cattle, especially of new-born calves), *Haemophilus influenzae* (a cause  
cc of meningitis), *Neisseria gonorrhoeae* (a cause of gonorrhoeae), *Yersinia*  
cc *enterocolitica* (the cause of a spectrum of disease in humans ranging  
cc from gastroenteritis to fatal septicaemic disease), *Bordetella pertussis*  
cc (the cause of whooping cough), and *Brucella abortus* (a cause of abortion  
cc and infertility in cattle and a condition known as undulant fever in  
cc humans).

Sequence 367 AA;

Query Match 98.08; Score 1914; DB 20; Length 367;

Best Local Similarity 98.18; Pred. No. 1.9e-145;  
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0

Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	MSKSLALLIPALLAAGAHAAEVYNNKDNKLNLDLYGKVDGLHYSNDKNVDGDOTYMRIG	60
	1		
	1	mkvkvslilvpaillvaagaanaeevynkdxmldlygkvdglnhyscnkdyvqdaqclymrlg	60
Db			
QY	61	FKGEGVTIDQLTGYGOWEYQIQGNSAENENNSWTRVAFAGLKFPDVCSPFYGRNRYGVYD	120
Db	61	fkgeqlvrdqtlgygqweyqlqgnsaeeennswrrvaftaglkfcdvgsfdygrnrygvvd	120
QY	121	VTSMTDVLPREGGPTTGSNDNMQORGNFGATYRRTDFFGLVDGLNFVAVQIQGKNKNSGE	180
Db	121	vtswtdvlpreggpttgsndnmqorngnfngatyrtrtdffglvldglnfvaavgqknpsge	180
QY	181	GFTSGVYNNNGSDALRONGDVGSGSITDYDEGFGIGAISSSKRPDAONTAAVIGNEBRAE	240
Db	181	gfetsgvchnrgdaltreqngdvvgssiltidydegfglgaisskskrtdaontaaylgnqrae	240
QY	241	TYTSGGLKYDANNIYLAAQYOTYVNAATRVGSLGMANKQONEFAVAQYOFDGLRPSLYIQ	300
Db	241	tytsglkydanniylaegybcqlytaatrvgslgmwnkneqnteaavayqfdcgilrpslaylq	300
QY	301	SKGNRLGKGYDDEILIKYVDGATYYRNKNKSTYYVDKINLDDNQFTTRAGINTDNIVA	360
Db	301	skgnrlgryyddedilikyvdgalyfinkmstyyvdyklnlldnqftrdagintdniva	360
QY	361	LGILVYOF 367	
Db	361	lgilvyqf 367	

## RESULT 2

ID AAY34058 standard; protein; 367 AA.

AC AAY34058;

DT 23-NOV-1999 (first entry)

DE E. coli outer membrane protein c precursor.

KM ulcerative colitis; histone; H1-like antigen; porin antigen;  
KM Bacteroides antigen; IBD; PANCA; inflammatory bowel disease;  
KM diagnosis: perinuclear anti-neutrophil cytoplasmic antibody;

KW outer membrane protein c precursor.

OS Escherichia coli.

PN W09945955-A1.

PD 16-SEP-1999.

PF 12-MAR-1999; 99WO-US05492.

PR 12-MAR-1998; 98US-0041889.

PA (REGC ) UNIV CALIFORNIA.

PI Braun J, Cohavy O;

DR WPI; 1999-551215/46

PT Use of histone H1, porin or Bacteroides antigens as targets for the  
PT diagnosis, prevention and treatment of ulcerative colitis -

PS Claim 8; Fig 11; 134pp; English.

CC The invention provides a method for the diagnosis, prevention and  
CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a  
CC porin antigen or a Bacteroides antigen as a target antigen. The novel  
CC method of diagnosing UC in a subject suspected of having inflammatory  
CC bowel disease (IBD) comprises: (1) obtaining a sample from the subject;  
CC (2) contacting the sample with a histone H1-like antigen, or perinuclear  
CC anti-neutrophil cytoplasmic antibody (pANCA)-reactive fragment, to form a  
CC complex of the histone H1-like antigen, or the pANCA-reactive fragment,  
CC and antibody to the histone H1-like antigen; and (3) detecting the  
CC presence or absence of the complex; where the presence of the complex  
CC indicates that the subject has UC. The pANCA-reactive histone H1-like  
CC antigen, porin antigen and Bacteroides antigen are useful in the  
CC diagnosis, prevention and treatment of UC. The methods can also be used  
CC for identifying agents useful for treating UC. The present sequence  
CC represents a E. coli outer membrane protein c precursor.

**SQ** Sequence 367 AA;

Query Match	98.0%	Score 1914	DB 20	Length 367
Best Local Similarity	98.1%	Pred. No. 1.9e-145		
Matches 360	Conservative 3	Mismatches 4	Indels 0	Gaps 0

QY	1	MKSVMKLLDLPALLAAGAAHAEEVYKRDKNKLDLYGKVDGLHYPSSDKKDVGDQDTYMRIG	60
	1		
	1	mkvav1ellvpa11vagaanaaevyndgknl0dlygvvdqjhytsdhkktvdqdcqlymr1g	60
Db	1		
QY	61	FKGETVTDLTGTGQWERYIQGSAENENNSWTRVAPAGLKFDQVGSFDPYGRNYGVYD	120
Db	61	fkgetvtdqltgyrgweyqjgnsaenenswtrvafaglkfdqvsfdygrnygvvyd	120
QY	121	VTSMWDLVPFEGSGFTYSSDNPMOGRGNFATYRNTDFEGLVDGLNFAVOYQGRKNGNSGE	180
	121		
Db	121	vtsmwdlvpfegsgftysdnpmoorgnfnatyrntdfeglvdglnfvayqygrknpsge	180
QY	181	GFETSGVNNNGDALARONGDDVGSGITVYDEFGFGIGSAISSKRPDAONTAAYIGNGRAE	240
Db	181	gfetsgvnnngdalarongddvggsiltvdyegfg1ggaisskrtdaqncaay1gngdrae	240
QY	241	TYTSGGLKYDANNITLAAYOTYNAATRVGSLGMANKAKONEEAAVAYOFDFGLRPSLAIYQ	300
	241		
Db	241	tytsglkydannitlaayotyntaatrvgslgmankakoneeaaavyofdfglrpslaiyq	300
QY	301	SKGKNLGRGYDDEDILKYVDVGATYFNKNMSTVYDYKINLLDNDQETFRDAGINTPDNIVA	360
	301		
Db	301	skgknlgryyddedilkyvdvagatlyfnknmstvydykinlldndqetfrdagintpdniva	360
QY	361	LGATYQF 367	
	361		
Db	361	lgatlyqf 367	

	RESULT	3	
AA57356	ID	AA57356 standard; Protein: 367 AA.	
XX	AC	AA57356;	
XX	DE	13-JUN-2000 (first entry)	
XX	PE	E. coli outer membrane protein c precursor.	
XX	PM	Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb;	
XX	RW	PANCA; perinuclear anti-neutrophil cytoplasmic antibody;	
XX	KW	histone H1; outer membrane protein c precursor.	
OS	ES	Escherichia coli.	
XX	PD	USG033864-A.	
XX	PF	07-MAR-2000.	
XX	PI	12-MAR-1998; 98US-0041889.	
XX	PR	12-APR-1996; 96US-0057846.	
XX	PT	11-APR-1997; 97US-0837058.	
PA	(REGC ) UNIV CALIFORNIA.		
XX	Cohavy O, Braun J;		
DR	WPI; 2000-255695/22.		
XX	Diagnosing ulcerative colitis or susceptibility, by detecting complex		
PT	formation between microbial porin antigen and perinuclear		
PT	anti-neutrophil cytoplasmic autoantibodies -		
PS	Claim 1; Fig 10; 49pp; English.		
XX	The invention provides a method for diagnosing ulcerative colitis in a		
CC	subject suspected of having inflammatory bowel disease. The method		
CC	comprises reacting a patient sample with a porin antigen that is		
CC	immunologically reactive with PANCA (perinuclear anti-neutrophil		
CC	cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex		
CC	as indicative of ulcerative colitis. The method is used to diagnose		
CC	ulcerative colitis or susceptibility to it. The present sequence		
CC	represents a E. coli outer membrane protein c precursor.		
XX	Sequence 367 AA:		
SQ			
	Query Match	98.0%; Score 1914; DB 21; Length 367;	
	Best Local Similarity	98.1%; Pred. No. 1.9e-145;	
	Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
OY	1	MKSKVIALIIPLLAAGAAHAEVYNKKGNKRLDGKVUGLHYFSPNKNVDDQDTMRIG	60
Dd	1	mkvkxslilvpallvagaanaaevyknkdnllygkyvgllhyfsdnkvdqqlymrig	60
OY	61	FKGEVQVVDOLGLGYGOMEXYOIQNGSNAEENNNNSMTFAAFGLKFODGSDFYCRNTGVVD	120
Dd	61	fkgexqvddqltlygyqwqwyqigsnaeenmswtvtvaefglkfcdygsldyrnygvvyd	120
OY	121	VTSWTDVLPERGGDTPGSDFNQMGNGFCATRYRTDFGLVDGLNFANOYCKRGNSPGE	180
Dd	121	vtswdvlpeirggdtlpgysdnlmqrgnfatyrndffglvdklnfavyg9gknpsge	180
OY	181	GFTSGVTNNGRDALBONGDVGSGSTTYDEEGGIGAISSSRKTPAOONAAATIGNDBRAE	240
Dd	181	gfstsvtnmgrdalrqnngdyvsgsltyldegfgyiggaissksrrtdagntaaayigngdrae	240
OY	241	TYTGGLEKTANNIYLAAOYTOTYTNATRVGSLGWANKAQNFEAVAOYOFDFGLRPISLAYIQ	300

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Db      241  tytggklykdanniyiaaqtgctqymatrrgsjswankacqnfavevaqyqgfifglrpsajyq 300
QY      301  SSGKNLGRDYDEEDILKYVDVGAITYYFNKNMSTYYDYKINLLDDNQETFRDAGINFDNIVA 360
      |||||||
Db      301  skgkmlgrgydeddillkyvdgatytfknkmstydckinlliddnqftrdagintdniva 360
QY      361  LGLVYQF 367
      |||||||
Db      361  lglvyqf 367
      |||||||

RESULT 4
ID      AAY34057 standard; protein; 377 AA.
AC      AAY34057;
XX      AAY34057;
DT      23-NOV-1999 (first entry)
DE      E. coli outer membrane protein F precursor.
KW      Ulcerative colitis; histone; H1-like antigen; porin antigen;
KW      Bacteroides antigen; IBD; PANCA; inflammatory bowel disease;
KW      diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;
KW      outer membrane protein F precursor.
XX      Escherichia coli.
XX      OS
XX      WO9945955-A1.
PN      16-SEP-1999.
PD      12-MAR-1999; 99WO-US05492.
PF      12-MAR-1998; 98US-0041889.
PR      (REGC ) UNIV CALIFORNIA.
XX      PA
XX      Braun J, Cohavy O;
XX      WPI: 1999-551215/46.
XX      Use of histone H1, porin or Bacteroides antigens as targets for the
PT      diagnosis, prevention and treatment of ulcerative colitis
XX      Claim 8; Fig 11; 134pp; English.
XX      The invention provides a method for the diagnosis, prevention and
XX      treatment of ulcerative colitis (UC) using histone H1-like antigen, a
CC      porin antigen or a Bacteroides antigen as a target antigen. The novel
CC      method of diagnosing UC in a subject suspected of having inflammatory
CC      bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
CC      (2) contacting the sample with a histone H1-like antigen, or perinuclear
CC      anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a
CC      complex of the histone H1-like antigen, or the PANCA-reactive fragment,
CC      and antibody to the histone H1-like antigen; and (3) detecting the
CC      presence or absence of the complex; where the presence of the complex
CC      indicates that the subject has UC. The PANCA-reactive histone H1-like
CC      antigen, porin antigen and Bacteroides antigen are useful in the
CC      diagnosis, prevention and treatment of UC. The methods can also be used
CC      for identifying agents useful for treating UC. The present sequence
CC      represents a E. coli outer membrane protein F precursor.
XX      SQ
XX      Sequence 377 AA;

Query Match 65.8%; Score 1285; DB 20; Length 377;
Best Local Similarity 67.3%; Pred. No. 4.5e-95;
Matches 259; Conservative 38; Mismatches 62; Indels 26; Gaps 10;

1 MMSKVALLIPALLAAGAAHAAYNNKDGKLDLYGKVDGLHYFSDNKNKDVDCDQTYMRIG 60.
|||||
1 msksvallipallaaagaahaeaynnkdgnkldlygvdgvlhyfidsnaksdgdgsyarlg 60

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CC	(AAZ22889-222893) to produce a non-reverting deletion mutation. The
CC	mutant ompF gene (AAZ22888) was used in the production of a bacterium
CC	attenuated by a non-reverting mutation in each of the ompF gene, the arcC
CC	gene (AAZ22883), AAZ22884), and the ompC gene (AAZ22885, AAZ22886). The
CC	mutant bacteria provide immunogenic activity with reduced virulence and
CC	thus can be used as a vaccine for raising an immune response against a
CC	variety of bacteria in a mammalian host. Such vaccines can provide
CC	protection against e.g., E. coli (a cause of diarrhoea in humans),
CC	Salmonella typhimurium (the cause of salmonellosis in several animal
CC	species), S. typhi (the cause of human typhoid), S. enteritidis (a cause
CC	of food poisoning in humans), S. choleraesuis (a cause of salmonellosis
CC	in pigs), S. dublin (a cause of both a systemic and diarrhoeal disease in
CC	cattle, especially of new-born calves), Haemophilus influenzae (a cause
CC	of meningitis), Neisseria gonorrhoeae (a cause of gonorrhoeae), Yersinia
CC	enterocolitica (the cause of a spectrum of disease in humans ranging
CC	from gastroenteritis to fatal septicemic disease), Bordetella pertussis
CC	(the cause of whooping cough), and Brucella abortus (a cause of abortion
CC	and infertility in cattle and a condition known as undulant fever in
XX	humans).
SX	
SX	Sequence 362 AA:
Query Match	56.5%; Score 1104; DB 20; Length 362;
Best Local Similarity	58.9%; Pred. No.1.3e-80;
Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;	
OY	1 MKSKVLALLIPLLAAGAAHAEVYNKRGKNKLDTYGKVDGLHYFS-----DNKKVDGDOT 55
Dd	2 mkrnlavlpallvagatanaaeIynkqknkvdiLygkaagvlyIskgngensyggngdnt 61
OY	56 YMRLEFKETQYTDDLTGTGWMEYOIQGSABEN---ENNSTRVAFAFLKFODVSFPVG 112
Dd	62 yarlfkgctqinsdltyggsgweyftfgnnsagaqaqgnkrrlafagkykdavgstfyg 121
OY	113 RNYGVYDVTSMTDVLPFRFGDPTYSNDNFMQGRNFATYRNTDFEGLVDGINPAVOYOG 172
Dd	122 rnygvvydalgytldlpefjgdtaysdftfygrvgvatlyrnsnltfyldvgtinfavylg 181
OY	173 KNGNSGGSGFTSGVYNNGNRD-ALRONGCGVGSIITYDEGFICGAISSKRTRDOQNPA 231
Dd	182 k-----nerdcarrngdgvgvgsisyeyegfiyvaayaadtntlqe-aq 225
OY	232 YINGDRARETYTGILKYDANNITYYLAOYTQTYNATR-----GSLGMWKAONFEAVAY 286
Dd	226 plngskkxaeqwtgkydanmilylaanygetnatpllnkfntsgfanktgdvillyaqy 285
OY	287 QEPDELRSIAVLOSKGNLGRGYDDEDILKRVVDGATYYFFKNNSTVYDYKINILLD-DN 345
Dd	286 qrdfiglrpslactksakadv-egldvdvlvmfyevgatcyfinkmslvdytilingdsdn 344
OY	346 QPTRDAGINTDNIVALGLVYOF 367
Dd	345 kl----gygsddtvavglvyqt 362
RESULT 7	
ID	AAAY34056 standard; protein: 323 AA.
XX	AAAY34056;
XX	
DT	23-NOV-1999 (first entry)
XX	
DE	E. coli outer membrane protein F precursor.
KM	Ulcerative colitis; histone; H1-like antigen; porin antigen;
KM	Bacterioides antigen; IBD; PANCA; inflammatory bowel disease;
KM	diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;
KM	outer membrane protein F precursor.
XX	
OS	Escherichia coli.
XX	

PN		MO9945955-AI.	
XX			
PD		16-SEP-1999.	
XX			
PF		12-MAR-1999;	99WO-USO5492.
XX			
PR		12-MAR-1998;	98US-0041889.
XX			
PA		(RESC ) UNIV CALIFORNIA.	
PI		Braun J, Cohavy O;	
XX			
DR		WPI: 1999-551215/46.	
XX			
PT		Use of histone H1, porin or Bacteroides antigens as targets for the	
PT		diagnosis, prevention and treatment of ulcerative colitis	
XX			
PS		Claim 8; Fig 11; 134pp; English.	
XX			
CC		The invention provides a method for the diagnosis, prevention and	
CC		treatment of ulcerative colitis (UC) using histone H1-like antigen, a	
CC		porin antigen or a Bacteroides antigen as a target antigen. The novel	
CC		method of diagnosing UC in a subject suspected of having inflammatory	
CC		bowel disease (IBD) comprises: (1) obtaining a sample from the subject;	
CC		(2) contacting the sample with a histone H1-like antigen, or perinuclear	
CC		anti-neutrophil cytoplasmic antibody (panCA)-reactive fragment, to form a	
CC		complex of the histone H1-like antigen, or the panCA-reactive fragment,	
CC		and antibody to the histone H1-like antigen; and (3) detecting the	
CC		presence or absence of the complex; where the presence of the complex	
CC		indicates that the subject has UC. The panCA-reactive histone H1-like	
CC		antigen, porin antigen and Bacteroides antigen are useful in the	
CC		diagnosis, prevention and treatment of UC. The methods can also be used	
CC		for identifying agents useful for treating UC. The present sequence	
CC		represents a E. coli outer membrane protein F precursor.	
XX			
SO		Sequence 323 AA:	
	Query Match	55.2%; Score 1078.5; DB 20; Length 323;	
	Best Local Similarity	66.2%; Pred. No.1.2e-78;	
	Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps		9;
OY	1	MKSVALALLIPALLAAGAAHAAEYNNKDGKIDLGYKVDGLHYFSDNKKDVGDQTYMRIG	60
DB	1	mksvalallipalllaagaaahaeaynnkdgkidlgykvqdlhyfidsnakdgdgsyarlg	60
OY	61	FKGEQVVDLTGVCOWMYEQIOGSNAE-NENNSMTVRVAFAGLKFDDYSFDXGRNVGVY	119
DB	61	fkgvqvndqlgygqwewyinnqnntesskngswrltlaaglkfdysfdfgrnyymy	120
OY	120	DVTSMTDLPFFEGSDTY-GSDNFMOORNFEGATYENTDFEGLVDGLINFAVOYOGRNGNPS	178
DB	121	dvgvtdmlpfegsdtytnadnfmrgangvatyntdfifglvnglnfvayqgnn---	176
OY	179	GEGFTSGV--TNNGDALRQNDGVGSGITTYDY-RGFGTGAISSSKRTRDAO--NTAAYI	233
DB	177	-egaanagegtungtcdrvhengdgvylstlylmgfsagaaytsddrtundvnhltaa--	233
OY	234	GNGDAEERYTGGLKADANNIYLAAOTYTQYNTRYGSLGW--ANKAONFEAAVOYQPDFG	291
DB	234	-ygdaadaawtglikydannilylatmnysetrmtpbgdsdyvaanktqnfveasyqfidg	292
OY	292	LRPSTLAYLOSKGNKL-----GGGYDED 314	
DB	293	lrpavsfmskygrdlhaagagdnpagvdckd 323	
RESULT	8		
AAI57354	ID	AAI57354 standard; Protein: 323 AA.	
XX			
AC		AAI57354;	
XX			

DT 13-JUN-2000 (first entry)  
 XX E. coli outer membrane protein F precursor.  
 XX  
 XX  
 XX ulcerative colitis; inflammatory bowel disease; porin antigen; Mab;  
 KM PANCA; perinuclear anti-neutrophil cytoplasmic antibody;  
 KM histone H1; outer membrane protein F precursor.  
 XX  
 XX Escherichia coli.  
 OS  
 XX US6033864-A.  
 PN  
 XX 07-MAR-2000.  
 PD  
 XX  
 XX 12-MAR-1998; 98US-0041889.  
 PF  
 XX  
 XX 12-APR-1996; 96US-0057846.  
 PR 11-APR-1997; 97US-0837058.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Cohavy O, Braun J;  
 PI  
 XX WPI; 2000-255695/22.  
 DR  
 XX  
 XX Diagnosing ulcerative colitis or susceptibility, by detecting complex  
 PT formation between microbial porin antigen and perinuclear  
 PT anti-neutrophil cytoplasmic autoantibodies -  
 XX  
 XX Claim 1, Fig 10; 49pp: English.  
 PS  
 XX  
 XX The invention provides a method for diagnosing ulcerative colitis in a  
 CC subject suspected of having inflammatory bowel disease. The method  
 CC comprises reacting a patient sample with a porin antigen that is  
 CC immunologically reactive with PANCA (perinuclear anti-neutrophil  
 CC cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex  
 CC as indicative of ulcerative colitis. The method is used to diagnose  
 CC ulcerative colitis or susceptibility to it. The present sequence  
 CC represents a E. coli outer membrane protein F precursor.  
 CC  
 XX  
 XX Sequence 323 AA;  
 SQ

Query Match 55.2%; Score 1078.5; DB 21; Length 323;  
 Best Local Similarity 66.2%; Pred. No. 1.2e-78;  
 Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

QY 1 MKSKVIALIPALLAAGAAHAAEVYKNDGKLDLYGKVDGLHFSNDKVDGQOTYWRIG 60  
 |||||||  
 DB 1 mkskvialipallaaagaahaaevynkdgnkldlygkvdlhyfshnsakdgqsyarlq 60  
 |||||||  
 QY 61 FKGETVTDLTGYGOWEYOIGNSAE-NENNSWTRVAFAGLKFODVGSFDRNGVYV 119  
 |||||||  
 DB 61 fkegetvtdltgygoweoyoignsaenennswtrvafaglkfodvgsfdrnrvyvy 120  
 |||||||  
 QY 120 DVTSMWTDVLPREFGDTY-GSDNFMQORNGFNATRYNTDFEGLVDGLNFAVOYOGKNGNPS 178  
 |||||||  
 DB 120 dvtswtdvlprefgdyt-gsdnfmqorngfnatryntdfeglvnglnfayvqygnn- 176  
 |||||||  
 QY 179 GEERTGV--TNGRDLALRNGDVGSGSTYDY-BEGFGIGALSSSKRTDAQ--NTAAYI 233  
 |||||||  
 DB 179 geertgv--tnggrdlalrngdvgsgsttydy-begfgigalssskrtdaq--ntaayi 233  
 |||||||  
 QY 234 GNDRAETVYTGGLKYDANNIYLAQYOTYNATRVGSLGW--ANKKQNFPAVAYQOFDFG 291  
 |||||||  
 DB 234 gndraetvtytgglkydanniylaqyotynatrvvgslgw--ankkqnfpaavayqofdfg 292  
 |||||||  
 QY 292 LRPFLAYLQSKGNL-----GREGDDED 314  
 |||||||  
 DB 292 lrpvafllmskgrdlhaagadnpagvddkd 323  
 |||||||  
 RESULT 9

AAW92998  
 ID AAW92998 standard; protein; 340 AA.  
 XX  
 XX AAW92998;  
 AC  
 XX  
 XX 19-MAY-1999 (first entry)  
 DT  
 XX  
 XX E. coli OmpF porin protein.  
 DE  
 XX  
 XX OmpF; porin; amphiphilic alpha-structure; beta-structure; GLUT;  
 KM membrane protein; glucose transporter protein; function.  
 KM  
 XX Escherichia coli.  
 OS  
 XX WO9618957-A1.  
 PN  
 XX  
 XX 20-JUN-1996.  
 PD  
 XX  
 XX 13-DEC-1995; 95WO-US16126.  
 PF  
 XX  
 XX 14-DEC-1994; 94US-0355844.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Cheung M, Czegledy F, Fischbarg J, Iserovich P;  
 PI Li J;  
 PI  
 XX WPI; 1996-300839/30.  
 DR  
 XX  
 XX Predicting tendency to form amphiphilic alpha and beta structures -  
 PT using a novel algorithm to calculate values for subsequent graphical  
 PT analysis to predict protein structure  
 XX  
 XX Disclosure; Fig 2; 106pp: English.  
 PS  
 XX  
 XX This invention describes a novel method for predicting the tendency of  
 CC a protein to form either: (a) an amphiphilic alpha-structure or (b) an  
 CC amphiphilic beta-structure. The methods are used particularly for  
 CC predicting the structure of membrane proteins such as glucose transporter  
 CC proteins (GLUTs). They can be used to discern the function of proteins.  
 CC They can also be used for the rational design or identification of  
 CC compounds which interact with the proteins or to engineer proteins having  
 CC particular structures. This sequence represents an Escherichia coli  
 CC OmpF porin which is used to illustrate the method of the invention.  
 CC  
 XX  
 XX Sequence 340 AA;  
 SQ

Query Match 52.6%; Score 1027; DB 17; Length 340;  
 Best Local Similarity 58.4%; Pred. No. 1.8e-74;  
 Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEYVNDGKKLDLYGKVDGLHFS-----DNKDVDDQOTYMRGFEGETVTDLTGYGQ 76  
 |||||||  
 DB 1 aelyvndgkkldlygkvdlhyfshnsakdgqsyarlq 60  
 |||||||  
 QY 77 WEYOIGNSAEN---ENNSWTRVAFAGLKFODVGSFDRNGVYDVTSMWTDVLPREFG 133  
 |||||||  
 DB 77 weyoignsaen---ennswtrvafaglkfodvgsfdrnrvyvydvtswtdvlprefg 120  
 |||||||  
 QY 134 DTYGSDNFMQORNGFNATRYNTDFEGLVDGLNFAVOYOGKNGNPSGEGTSCVTNNGRP- 192  
 |||||||  
 DB 134 dtygsdnfmqorngfnatryntdfeglvnglnfayvqygnn- 165  
 |||||||  
 QY 193 ALRONGDVGSGSTYBEGFGIGALSSSKRTDAQNTAAYTGNGDRAETVYTGGLKYDANN 252  
 |||||||  
 DB 193 alrongdvgsgsttybegfgigalssskrtdaqntaaytgngdraetvtytgglkydann 224  
 |||||||  
 QY 253 IYLAQYOTYNATRV-----GSLGNANKQNFPAVAYQOFDFGLRPLSLAYLQSKGNLIG 307  
 |||||||  
 DB 225 iylaanygetnatrvpntkftntsfanktqdvllvaqyqdfgflrpslaylqskskadv- 283  
 |||||||  
 QY 308 RGIDDEDILKYVDVGAITYYFNKMKSTYVYDKINLND-DNQFTRDAGINTNDVALGLVYQ 366  
 |||||||

	Matches	45;	Conservative	10;	Mismatches	16;	Indels	5;	Gaps	1
OY	1	MKSKVLLALLPALLAAGAAHAEVYNKRDKNLDTYGRVDGLHYTS-----DNKKVDGPOT	55							
		: : : :         : :     : :                                 : : :								
Db	2	mkrlllavivgallvagtanaaaelynkdkgnkvddlygkavglhtxfskngensyngngdnt	61							
OY	56	YMRIGFKEGTQVTDPQL	71							
Db	62	yarlfgfgetqxnsl	77							
	RESULT	11								
	AAY26025									
ID	AAV26025	standard; Protein; 353 AA.								
XX	AAV26025;									
AC	AAV26025;									
DT	29-SEP-1999	(first entry)								
XX										
DE	OmpH protein of H.influenza porin P2.									
XX										
KW	Pouter membrane protein H: ompH gene; fowl cholera; molecular sieve;									
KM	Bacterial porin, X-73; porin; avian; vaccine; veterinary medicine;									
KM	bacterial porin, H.influenzae porin P2.									
OS	Haemophilus influenzae.									
PN	WC0929724-A2.									
XX										
PD	17-JUN-1999.									
PF	08-DEC-1998;	98WO-US25990.								
XX										
PR	21-JUL-1998;	98US-0120051.								
XX	08-DEC-1997;	97US-0067957.								
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.									
PI	Glisson JR, Luo Y;									
DR	WPI; 1999-385575/32.									
PT	DNA encoding Pasteurella multocida outer membrane protein H, useful									
PS	for delivering peptide epitopes for vaccines against fowl cholera									
PS	Disclosure; Fig 5; 11pp; English.									
CC	The present amino acid sequence is that of the Haemophilus influenzae									
CC	porin P2. This protein is a bacterial porin, which is a major outer									
CC	membrane protein that is involved in pore formation. They serve as									
CC	molecular sieves that allow polar solutes to pass through, but excludes									
CC	non-polar molecules of comparable sizes. This amino acid sequence shares									
CC	a sequence homology of about 38% to Pasteurella multocida X-73 OmpH									
CC	protein. Peptides derived from the P.multocida OmpH protein are useful									
CC	in the production of protective vaccines for use in vertebrates in									
CC	particular, for prevention of fowl cholera and for diagnosis in									
CC	veterinary medicine.									
SQ	Sequence	353 AA;								
	Query Match	9.6%; Score 187.5; DB 20; Length 353;								
	Best Local Similarity	21.9%; Pred. No. 2.9e-07;								
	Matches	89; Conservative	53; Mismatches	126; Indels	139; Gaps	16;				
OY	4	KVALLPALLAAGAHAHAEEVYNKRDKNLDLYGKV-----	38							
Db	3	kllaalivgaafaasanaaavynegtvelgvrsvlaaeqstsnrkdkqhqsrlrng	62							
OY	39	-----DG---LHYFSD---NKDVDGDQTVMRLKGFGEMGYTDQLTGVGGWEYG	80							
Db	63	srfnlkvtnlmgdyayagyyetctfnklidgneknlgsgtgsilt-----	107							





PT for delivering peptide epitopes for vaccines against fowl cholera  
 XX Claim 12; Fig 11; 119pp; English.  
 XX  
 CC The present amino acid sequence is that of the avian Pasteurella  
 CC multocida P-1059, outer membrane protein H (OmpH). This protein is a  
 CC porin, which is a major outer membrane protein that is involved in  
 CC pore formation. They serve as molecular sieves that allow polar solutes  
 CC to pass through, but excludes non-polar molecules of comparable sizes.  
 CC The amino acid composition is typical of non-specific bacterial porins  
 CC with highly negative hydropathy index, high glycine content, low proline  
 CC content and lack of cysteine. Multiple antigen peptides are synthesised  
 CC from the loop 2 and loop 5 regions of the protein that can be used for  
 CC immunisation of the fowls to induce heterologous protection against  
 CC P. multocida infection. This sequence can be used for diagnostic assays  
 CC for use in veterinary medicine, especially for the diagnosis of fowl  
 CC cholera, caused by P. multocida. Peptides derived from the OmpH protein  
 CC are useful in the production of protective vaccines for use in  
 CC vertebrates, in particular for prevention of fowl cholera.  
 XX  
 SQ Sequence 343 AA:  
 Query Match 8.9%; Score 174; DB 20; Length 343;  
 Best Local Similarity 22.9%; Pred. No. 3,4e-06;  
 Matches 96; Conservative 50; Mismatches 145; Indels 128; Gaps 18;  
 QY 1 MRSKVALIIPALLAAGAAHAEVYNNKDKLDLYGKVDGLHFSDNKVDGQDTYRLG 60  
 DB 1 mktliyalav-aavaatsnaatyngdgtkvngsvllllkkenergdldvngsrvs 59  
 QY 61 FKGEQVDTOLGTYGQWERYIOGN-----SAENE-----NNSWTRVAFAGLK 102  
 DF 60 fksahlgeglalsalayaaelrfsknekevkdqngvvrkyeverigndvhvkrlyagfa 119  
 QY 103 FQDVGSFEDYGRNNGVYDVTSWTDVLPFEFGDPTYSNDNMQRNGAAYRNDFEGLVD 162  
 DB 120 yeglgeltgnqlt-----gddvgsdy-----ty----- 145  
 QY 163 GLNFAYOYOGKGNPSEGFSGVTNNGRDALRQNGDVGSGITTYDEFGIGAISSSK 222  
 DB 146 -----flggin-----llsgekaifksaefngftggayvfs- 180  
 QY 223 RFDQAQTAAYIGNGRAEYTYTGL---KYDANNITYAAQYOTQYNAFRVSGSLGWAKAQN 279  
 DB 181 -adadqaprdqg----fvaglynrkmqdvqfalaegysqky---vtaakgekeka 231  
 QY 280 FEAVNAYQDFGRPSLALQSKGN-----LGRGVDEDEILK-YVD----- 320  
 DB 232 fmvgtelisy-agialgvdyagskvtrveggktralevglyndlkakvytdllwkegpk 290  
 QY 321 -----VGATYFFNKMSTYVDYKINLDDNOFTBDA-GINT-DNIVALGLYQF 367  
 DB 291 gattirsrillagaykllhqvelfvegwgvr-----ekdangvtlkkhkvgyglivhf 343  
 RESULT 14  
 ID AAY26023  
 AAY26023 standard; Protein; 353 AA.  
 XX  
 AC AAY26023;  
 XX  
 DT 29-SEP-1999 (first entry)  
 XX  
 DE OmpH protein of Pasteurella multocida X-73.  
 XX  
 KM Outer membrane protein H; ompH gene; fowl cholera; molecular sieve;  
 KM Pasteurella multocida X-73; porin; avian; vaccine; veterinary medicine;  
 KM bacterial porin; H influenzae porin P2.  
 XX  
 OS Pasteurella multocida.  
 XX  
 FH Key Location/Qualifiers

FT Peptide 1..20  
 FT /label= Signal\_peptide  
 FT /note= "Hydrophobic amino acids"  
 FT Protein 21..353  
 FT /note= "mature OmpH protein"  
 FT Cleavage-site 7..9  
 FT /note= "Present within the signal peptide"  
 FT Cleavage-site 9..11  
 FT /note= "Present within the signal peptide"  
 FT Cleavage-site 12..14  
 FT /note= "Present within the signal peptide"  
 FT Cleavage-site 18..20  
 FT /note= "Present within the signal peptide"  
 FT Peptide 81..110  
 FT /label= MAP-12-peptide  
 FT /note= "Multiple Antigen Peptide derived from loop 2"  
 FT Peptide 217..238  
 FT /label= MAP-15-peptide  
 FT /note= "Multiple Antigen Peptide derived from loop 5"  
 XX  
 XX W09929724-A2.  
 XX  
 XX PN 17-JUN-1999.  
 XX PD 08-DEC-1998; 98WO-US25990.  
 XX PF 21-JUL-1998; 98US-0120051.  
 XX PR 08-DEC-1997; 97US-0067957.  
 XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX PI Glisson JR, Luo Y;  
 XX WPI; 1999-385575/32.  
 XX DR N-PSDB; AAX80609.  
 XX  
 PT DNA encoding Pasteurella multocida outer membrane protein H, useful  
 PT for delivering peptide epitopes for vaccines against fowl cholera  
 XX  
 XX Claim 10; Fig 4; 119pp; English.  
 XX  
 CC The present amino acid sequence is that of the avian Pasteurella  
 CC multocida X-73, outer membrane protein H (OmpH). This protein is a  
 CC porin, which is a major outer membrane protein that is involved in  
 CC pore formation. They serve as molecular sieves that allow polar solutes  
 CC to pass through, but excludes non-polar molecules of comparable sizes.  
 CC The amino acid composition is typical of non-specific bacterial porins  
 CC with highly negative hydropathy index, high glycine content, low proline  
 CC content and lack of cysteine. This amino acid sequence shows homology of  
 CC about 38% to bacterial porins, like that of H. influenzae porin P2.  
 CC Multiple antigen peptides are synthesised from the loop 2 and loop 5  
 CC regions of the protein that can be used for immunisation of the fowls  
 CC to induce heterologous protection against P. multocida infection. This  
 CC sequence can be used for diagnostic assays for use in veterinary  
 CC medicine, especially for the diagnosis of fowl cholera, caused by  
 CC P. multocida. Peptides derived from the OmpH protein are useful in the  
 CC production of protective vaccines for use in vertebrates, in particular  
 CC for prevention of fowl cholera.  
 XX  
 SQ Sequence 353 AA:  
 Query Match 8.8%; Score 171; DB 20; Length 353;  
 Best Local Similarity 23.1%; Pred. No. 6e-06;  
 Matches 99; Conservative 48; Mismatches 144; Indels 138; Gaps 19;  
 QY 1 MRSKVALIIPALLAAGAAHAEVYNNKDKLDLYGKVDGLHFSDNKVDGQDTYRLG 60  
 DB 1 mktliyalav-aavaatsnaatyngdgtkvngsvllllkkenergdldvngsrvs 59  
 QY 61 FK-----GE-----TOYTDQLTGQWERYIOGSAENENNSWTRVAF 98  
 DB 60 fksahlgeglalsalayaaelrfsknvprvqkdq-ggevtrveve-----klgnvhvkrly 114





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 : Search time 12.29 Seconds  
(without alignments)  
614,862 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953

Sequence: 1 MKSKVLALLPALLAGAAH.....TRDAGINTDVALGLVYQF 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	3	US-09-041-889-30
2	1285	65.8	377	3	US-09-041-889-29
3	1078.5	55.2	323	3	US-09-041-889-28
4	1027	52.6	340	2	US-08-355-844-1
5	1027	52.6	340	5	PCT-US95-16126-1
6	164.5	8.4	361	4	US-08-096-181A-8
7	164.5	8.4	361	5	PCT-US94-08326-8
8	140.5	7.2	342	1	US-08-096-182A-4
9	140.5	7.2	342	1	US-08-877-109-4
10	140.5	7.2	342	3	US-08-798-760-4
11	140.5	7.2	342	5	PCT-US94-08327-4
12	140.5	7.2	363	1	US-08-096-182A-6
13	140.5	7.2	363	1	US-08-877-109-6
14	140.5	7.2	363	3	US-08-798-760-6
15	140.5	7.2	363	5	PCT-US94-08327-6
16	128.5	6.6	589	4	US-09-377-155-19
17	127.5	6.5	363	4	US-08-096-181A-10
18	127.5	6.5	363	5	PCT-US94-08326-10
19	126.5	6.5	342	4	US-08-096-181A-12
20	126.5	6.5	342	4	US-08-096-181A-14
21	126.5	6.5	342	5	PCT-US94-08326-14
22	124.5	6.4	511	1	US-08-480-604A-20
23	124.5	6.4	511	2	US-08-480-604A-21
24	124.5	6.4	608	1	US-08-405-496A-20
25	124.5	6.4	608	2	US-08-405-496A-21
26	124.5	6.4	608	2	US-08-480-604A-21
27	124.5	6.4	609	1	US-08-480-604A-30

28	124.5	6.4	2366	1	US-08-480-604A-10	Sequence 10, Appl
29	124.5	6.4	2366	2	US-08-405-496A-10	Sequence 10, Appl
30	118.5	6.1	309	1	US-08-096-182A-2	Sequence 2, Appl
31	118.5	6.1	309	1	US-08-877-109-2	Sequence 2, Appl
32	118.5	6.1	309	3	US-08-798-760-2	Sequence 2, Appl
33	118.5	6.1	309	5	PCT-US94-08327-2	Sequence 2, Appl
34	116.5	6.0	598	4	US-09-377-155-5	Sequence 5, Appl
35	116.5	5.8	592	4	US-09-377-155-17	Sequence 17, Appl
36	113.5	5.8	599	4	US-09-377-155-15	Sequence 15, Appl
37	112.5	5.8	594	4	US-09-377-155-7	Sequence 7, Appl
38	112.5	5.8	1657	3	US-09-057-570-2	Sequence 2, Appl
39	112.5	5.8	1805	3	US-09-057-570-7	Sequence 7, Appl
40	111.5	5.7	598	4	US-09-377-155-13	Sequence 13, Appl
41	111.5	5.7	3031	1	US-07-689-008-2	Sequence 2, Appl
42	110.5	5.7	591	4	US-09-377-155-11	Sequence 11, Appl
43	110.5	5.7	591	4	US-09-377-155-21	Sequence 21, Appl
44	110.5	5.7	592	4	US-09-377-155-2	Sequence 2, Appl
45	110	5.6	341	2	US-08-538-711A-8	Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-09-041-889-30  
; Sequence 30, Application US/09041889  
; Patent No. 6033864  
; GENERAL INFORMATION:  
; APPLICANT: Braun, Jonathan  
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/041,889  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/837,058  
; FILING DATE: 11-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-PM 3006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 367 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-041-889-30

Query Match 98.0%; Score 1914; DB 3; Length 367;  
Best Local Similarity 98.1%; Pred. No. 1.4e-157;  
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;



SEQUENCE CHARACTERISTICS:  
 LENGTH: 323 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-041-889-28

Query Match 55.2%; Score 1078.5; DB 3; Length 323;  
 Best Local Similarity 66.2%; Pred. No. 1.5e-85;  
 Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

QY 1 MKSVALLPALLAAGAAHAEVYNNKDGKLDYKVDGLHFRSDKVDGDOTYRLG 60  
 DB 1 MKSVALLPALLAAGAAHAEVYNNKDGKLDYKVDGLHFRSDKVDGDOTYRLG 60  
 QY 61 FKGEVOTDQITGQWEYDIOGNSAE--NENNSWTRVAFGLKRDQVGSFDYGNVGVY 119  
 DB 61 FKGEVOTDQITGQWEYDIOGNSAE--NENNSWTRVAFGLKRDQVGSFDYGNVGVY 119  
 QY 120 DVTSMTPDLPEFGGDTY--GSDNFMQGRNFGATYRNTDFGLVDGLNFAVOYOGKNGNPS 178  
 DB 121 DIEWTMTLPEFGSDSTNADNEMTGRANGVATYRNTDFGLVNGLNFAVOYOGSN---- 176  
 QY 179 GEGFTSGV--TNNGRDLRONGDVGSGITYDY--EGFGIGAISSSKRTDAQ--NTAAYI 233  
 DB 177 -EGASNGQESTNNGRDVREHNGDGMGLSTTYDLGMGFSAGAAYTSRDNDQVNHATA-- 233  
 QY 234 GNGRATYTGKLYDANNITYLAQYTOTYNATRVGSLGW--ANKAONFEVAVOYQDFG 291  
 DB 234 -GGKADAMTAGKLYDANNITYLATYSETRNMPFGSDSDYAVANKTONFEVTAQYQDFG 292  
 QY 292 LRPSLAVIOSKGNL-----GRGYDDED 314  
 DB 293 LRPAVSFLMSKGRDLHAAGADNPAGYDDKD 323

RESULT 4  
 US-08-355-844-1  
 ; Sequence 1, Application US/08355844  
 ; Patent No. 5940307  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischbarg, Jorge  
 ; APPLICANT: Czegledy, Ferenc  
 ; APPLICANT: Iserovich, Pavel  
 ; APPLICANT: Li, Jun  
 ; APPLICANT: Cheung, Min  
 ; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10112-0228  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/355,844  
 ; FILING DATE: 14-DEC-1994  
 ; CLASSIFICATION: 436  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Tang, Henry Y.S.  
 ; REGISTRATION NUMBER: 29,705  
 ; REFERENCE/DOCKET NUMBER: A29927-50/29910  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-408-2586  
 ; TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 340 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Escherichia coli  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..340  
 ; OTHER INFORMATION: OmpF porin protein  
 ; US-08-355-844-1

Query Match 52.6%; Score 1027; DB 2; Length 340;  
 Best Local Similarity 58.4%; Pred. No. 4.5e-81;  
 Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEVYNNKDGKLDYKVDGLHFRS-----DNKVDGDOTYMRLGFKGETVTDQITGYGQ 76  
 DB 1 AEIYNNKDGKVDLYKAVGLHYRSKGENSYGSGNDMTYARLGFKGETQINSIDLTGYGQ 60  
 QY 77 WEYDIOGNSAEN--ENNSWTRVAFGLKRDQVGSFDYGRNVGVYDVTSMTPDLPEFGG 133  
 DB 61 WEYDIOGNSAEN--ENNSWTRVAFGLKRDQVGSFDYGRNVGVYDVTSMTPDLPEFGG 120  
 QY 134 DTVSDFNFMQGRNFGATYRNTDFGLVDGLNFAVOYOGKNGNSGSGFTSGVYNNGRD- 192  
 DB 121 DTVSDFNFMQGRNFGATYRNTDFGLVDGLNFAVOYOGKNGNSGSGFTSGVYNNGRD- 165  
 QY 193 ALRONGDVGSGITYDYEGFGIGAISSSKRTDAQNTAAYINGDRATYTGKLYDANN 252  
 DB 166 ARSNGDVGSGISYEBGFGIYAGYADRTNQE--AQPLGNKKAQDMATGKLYDANN 224  
 QY 225 IYLAANYGETRNATPINKEFTNTSGFANKQDVLVAOYQDFGLRPSIAVTKSKARDV- 283  
 DB 225 IYLAANYGETRNATPINKEFTNTSGFANKQDVLVAOYQDFGLRPSIAVTKSKARDV- 283  
 QY 308 RGYDDEDILKLYDVGATYRNNKSTYVDYKINLDD--DNOFTTRAGINTDNYVALGLVYQ 366  
 DB 284 EGIQDVLVNFVEVGATYRNNKSTYVDYIINDISDNKL---GVGSDTVAVVGLVYQ 339  
 QY 367 F 367  
 DB 340 F 340

RESULT 5  
 PCT-US95-16126-1  
 ; Sequence 1, Application PC/TUS9516126  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischbarg, Jorge  
 ; APPLICANT: Czegledy, Ferenc  
 ; APPLICANT: Iserovich, Pavel  
 ; APPLICANT: Li, Jun  
 ; APPLICANT: Cheung, Min  
 ; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10112-0228  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Protein  
 TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Protein  
 TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Protein  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
 STREET: 1100 New York Avenue, Suite 600  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/096,181A  
 FILING DATE: 23-Jul-1993  
 CLASSIFICATION: 424  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 361 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match	8.4%;	Score 164.5;	DB 4;	Length 361;
Best Local Similarity	24.1%;	Pred. No. 1.4e-06;		

[illegible]

RESULT 7  
PCT-US94-08326-8  
Sequence 8, Application PC/TUS9408326  
GENERAL INFORMATION:  
APPLICANT: North American Vaccine, Inc.  
APPLICANT: 12103 Indian Creek Court  
APPLICANT: Beltsville, MD 20705  
APPLICANT: Pullen, Jeffrey K.  
APPLICANT: Soper, Thomas S.



1. APPLICANT: Liang, Shu-Mei  
2. TITLE OF INVENTION: A Method For The High Level  
3. TITLE OF INVENTION: Expression,  
4. TITLE OF INVENTION: Purification And Refolding Of The Outer Membrane  
5. TITLE OF INVENTION: Protein  
6. TITLE OF INVENTION: p2 From Haemophilus Influenzae Type b  
7. NUMBER OF SEQUENCES: 14  
8. CORRESPONDENCE ADDRESS:  
9. ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
10. STREET: 1100 New York Avenue, Suite 600  
11. CITY: Washington  
12. STATE: D.C.  
13. COUNTRY: U.S.A.  
14. ZIP: 20005-3934  
15. COMPUTER READABLE FORM:  
16. MEDIUM TYPE: Floppy disk  
17. COMPUTER: IBM PC compatible  
18. OPERATING SYSTEM: PC-DOS/MS-DOS  
19. SOFTWARE: Patent In Release #1.0, Version #1.25  
20. CURRENT APPLICATION DATA:  
21. APPLICATION NUMBER: PCT/US94/08326  
22. FILING DATE: Herewith  
23. CLASSIFICATION:  
24. PRIOR APPLICATION DATA:  
25. APPLICATION NUMBER: US 08/096,181  
26. FILING DATE: 23-JULY-1993  
27. ATTORNEY/AGENT INFORMATION:  
28. NAME: Esmond, Robert W.  
29. REFERENCE/DOCKET NUMBER: 1438.001PC01  
30. TELECOMMUNICATION INFORMATION:  
31. TELEPHONE: (202) 371-2600  
32. TELEFAX: (202) 371-2540  
33. INFORMATION FOR SEQ ID NO: 8:  
34. SEQUENCE CHARACTERISTICS:  
35. LENGTH: 361 amino acids  
36. TYPE: amino acid  
37. TOPOLOGY: linear  
38. MOLECULE TYPE: protein  
PCT-US94-08326-8

Query Match	8.4%	Score 164.5	DB 5	Length 361
Best Local Similarity	24.1%	Pred. No. 1.4e-06		
Matches 90	Conservative 52	Mismatches 145	Indels 87	Gaps 17

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QY      4 KVALLLPALLAAQAAHAAEYVNNKDGKMLDLGYVDGLHFESDKVDGQGYT----- 56
Db      3 KTLAALIVGFAAABAANAAVYNNNEGNNIVELGGSLTIAEOS--NSTYDNOKOCHGALRNQ 61
QY      57 -MRUGFGETQVTDLTGYGQMEYOIOGNSAENENNSM---TFVAFAGLKFDQVGSFDY 111
Db      62 GSRFHKATHNFGGGEFYAOGLETFRVYTKASENSDNGFQITTSKAVYVTLGNKAFFEVL 122
QY      112 GRNTGVYVDYTSWMDVLPBEGSGDTYSGDNFEQAKGN--FGATYRRTDFEGLVDGLNFVQY 170
Db      122 GRATTIADIGITSAD--KEYG--VLNNSDYIPTSNGNVGTETKID--GLVLEANY-- 171
QY      171 OGGKGNPSEGGEGTSGVTNNGRDALRQNGDGVGSGITDYEGFQIGCAISSSKRTDAONTA 230
Db      172 -----LLAQKREGAKG-----ENKRRNDKAGE 193
QY      231 AYIG--NGDRAETTYTGLKYDANNITLAAOYTQF--YANTRYGSLGWANKAQ--NFEA 282
Db      194 VRIGINGNGIDV-----GAKYDANDIVAKTAYAGRTNYKNESD-----EKKOOLNCVLA 242
QY      283 VAQYQF-DFGLRPSLAIQSGKKLWGAGCYDDEDLIKLYVDYGATYYFNKNNSTYVDYKI-- 339
Db      243 TLGRFSLDGLLVSLDSQYATKNTYKIKHEKR---YEVSPGEFQYELMEDINVYGNEFYER 299
QY      340 NILDDNOFTRDAGI 353
Db      300 TSVDDGEXTREDAV 313

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RESULT 8  
 US-08-096-182A-4  
 Sequence 4, Application US/08096182A  
 Patent No. 5439608  
 GENERAL INFORMATION:  
 APPLICANT: Blake, Milan S.  
 APPLICANT: Tai, Joseph Y.  
 APPLICANT: Qi, Huijin L.  
 APPLICANT: Liang, Shu-Mei  
 APPLICANT: Hronowski, Lucjan J.J.  
 APPLICANT: Pullen, Jeffrey K.  
 TITLE OF INVENTION: Method for the High Level Expression,  
 TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Protein B  
 TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
 STREET: 1100 New York Ave., Suite 600  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/096,182A  
 FILING DATE: 23-JUL-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 1438, 0060000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 342 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-096-182A-4

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Query Match      7.2%; Score 140.5; DB 1; Length 342;
Best Local Similarity 25.6%; Pred. No. 0.00015;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLFGKGETVDTDLGTYGOMEYOLOGNSAENENNISW-TRVAFAGLKFODVGSFEDGR--N 114
   ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 KIGFGAGDLDLGKMAIMQL- - - - - QKASIAGTNSGMWRNQSPFLGK-----GGFTVRAGN 95

QY 115 YGVY-----DYTSITDVLPFFGDTYSSDNFMQQRGNFGATYRTNTDFGL-----VDGL 164
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 96 LNTVLTKDSGDNNVAN- - - - - EESGNT-----EDVLGIOTIGRVESR 131

QY 165 NPAVOYGOKKNNGPSEGEFTSGV-----TNNGRDA-----LRONGDVGSIITYDEYGFGL 215
   ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 EISAVYD- - - - - SPVFAGSFSGYVPRONANDVKYKHTFKSSRESYHAAGLKENAGFPQG 187

QY 216 GAISSSK-----RTDAQNTAAVIGNDRAEY-----TGGLKDANNIY--LAAQYTQTVN 264
   ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 188 YAGSFARAKADLTNDTERARVAUNTANHPRKDIYOHRRVAG--YDANDLYVSAGQYEAAKN 245

QY 265 ATRVGSLL-GMANKAONFEAVNAOYOFDFGLRSLAYLIQS-KGKNILG--RGYDDDEDILKYV 319
   ||| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 -NEWGSTGKKHNEGQVAVATAAFYFRG-NVTTPRVSYAHGFKKAAVNQVKDANYQDQVI--- 300

QY 320 DVGATYYFNKKMNSTYV 335

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Db 132 EISVRD-----SPVFAGSGSVQYVPRDNANDYKRYKHTKSSRSYHAGLKYENAGFFGQ 187  
QY 216 GAISSSK-----RTDAONTAAYIGNGRAETV-----TGLKYDANNY--LAAQYTOTN 264  
Db 188 YAGSFAYADLNTDAEVAANTANAHFVKDYQVHRVYAG--TDANDLYVSAGQYEAKN 245  
QY 265 ATRVGS�-GMANKRQNEEAVAQYQDFGLRPSLAYLOS-KGNLQ---RGYDDEDILKYV 319  
Db 246 -NEVGSTKKGKHEQTOYAATAAYRFG-NVTPRVSYAHGFAYKAVGVANDANYQYDOYI--- 300  
QY 320 DVGATYFENKMSYV 335  
Db 301 -VGADYDFSKRTSALV 315

RESULT 11  
PCT-US94-08327-4

; Sequence 4, Application PC/TUS9408327  
; GENERAL INFORMATION:  
; APPLICANT: The Rockefeller University  
; APPLICANT: 1230 York Avenue  
; APPLICANT: New York, New York 10021  
; APPLICANT: United States of America  
; APPLICANT: 12103 Indian Creek Court  
; APPLICANT: Beltsville, Maryland 20705  
; APPLICANT: United States of America  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Qi, Hulin L.  
; APPLICANT: Liang, Shu-Mei  
; APPLICANT: Hironowski, Lucjan J.J.  
; TITLE OF INVENTION: Method for the High Level  
; TITLE OF INVENTION: Expression,  
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane  
; TITLE OF INVENTION: Group B  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08327  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/096,182  
; FILING DATE: 23 July 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.006PC00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 342 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US94-08327-4

Query Match 7.2%; Score 140.5; DB 5; Length 342;

Best Local Similarity 25.6%; Pred. No. 0.00015;  
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLGFKEQYTDLTGQWQYQIQGSAENENNSW-TRAFAGLKRFQDVGSPDYGR--N 114  
Db 43 KIGFGQEDLGNGKAIWOLE--QKASIAGTNSGWSGNRSFGLK---GGFGYVAGN 95  
QY 115 YGVVY-----DVSMVDLPEFGDGTYSQDNFMQQRGNFGATYRNDFFGL-----VDGL 164  
Db 96 LNTVLDGSDGNVANM-----ESGSNT-----EVLGLGTIGRVER 131  
QY 165 NFAVYQGNKNGPSGEGFTSGV-----TNCRDA-----LNQNDGCGSITTYDEGCGIG 215  
Db 132 EISVRD-----SPVFAGSGSVQYVPRDNANDYKRYKHTKSSRSYHAGLKYENAGFFGQ 187  
QY 216 GAISSSK-----RTDAONTAAYIGNGRAETV-----TGLKYDANNY--LAAQYTOTN 264  
Db 188 YAGSFAYADLNTDAEVAANTANAHFVKDYQVHRVYAG--TDANDLYVSAGQYEAKN 245  
QY 265 ATRVGS�-GMANKRQNEEAVAQYQDFGLRPSLAYLOS-KGNLQ---RGYDDEDILKYV 319  
Db 246 -NEVGSTKKGKHEQTOYAATAAYRFG-NVTPRVSYAHGFAYKAVGVANDANYQYDOYI--- 300  
QY 320 DVGATYFENKMSYV 335  
Db 301 -VGADYDFSKRTSALV 315

## RESULT 12

US-08-096-182A-6  
; Sequence 6, Application US/08096182A  
; Patent No. 5439808  
; GENERAL INFORMATION:  
; APPLICANT: Blake, Milan S.  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Qi, Hulin L.  
; APPLICANT: Liang, Shu-Mei  
; APPLICANT: Hironowski, Lucjan J.J.  
; APPLICANT: Pullen, Jeffrey K.  
; TITLE OF INVENTION: Method for the High Level Expression,  
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B  
; TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/096,182A  
; FILING DATE: 23-JUL-1993  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.0060000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 363 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-096-182A-6



```
REFERENCE/DOCKET NUMBER: 1438.0060002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-760-6

Query Match
Best Local Similarity 7.2%; Score 140.5; DB 3; Length 363;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLGFKEGTQYTDLTGCGWEYQIQNSAENENNSW-TRVAFAGLKFQDYGSEFDYGR--N 114
:||||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 KIGFKGEDLGNCKAIWOLE---QKASIAGTNSGNGRQSFGLK---GCGTVRAGN 116
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 YGVVY-----DVTSMIDVLEPFQGDYTGSDNFMQORGNFQATYRNDPGL-----VDGL 164
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 LNTVLKDSGDNVAM-----ESGNT-----EDVLGLGTIGRESR 152
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 NFAVOYQKNGNPSGEGFTSGV-----TNGRDA-----LRONGDVGGSITYDEGFGIG 215
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 153 EISVRD-----SPVFAFGSSVQYVPRDNANDVDKYKHTKSSRSYHAGLKYENAGFGQ 208
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 216 GAISSSK-----RTDAONTAAVINGNDRAETV-----TGILKYDANNIY--LAAQYTOTYN 264
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 YAGSFAKYADLNTDAERVAANTANAHFVKDYQVHRVYAG--YDANDLYVSAGQYEAAKN 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 265 ATRVGSU-GWANKAQNENVAOYQFDGLRPSLAYLOS-KGKNG---RGYDDEDILKYV 319
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 -NEVGSTGKGGKHETQVAAATPAATRFQ-NVTPRVSYAHGFAKAVNGVDANTQYDQVY--- 321
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 320 DVGATYYFNKNMSTYV 335
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 322 -VGADYDFSKRTSALV 336
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
PCT-US94-08327-6
Sequence 6, Application PC/TUS9408327
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
APPLICANT: 1230 York Avenue
APPLICANT: New York, New York 10021
APPLICANT: United States of America
APPLICANT: 12103 Indian Creek Court
APPLICANT: Beltsville, Maryland 20705
APPLICANT: United States of America
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Hulin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Hironowski, Lucjan J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level
TITLE OF INVENTION: Expression.
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane
TITLE OF INVENTION: Group B
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,182
FILING DATE: 23 July 1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.006PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08327-6

Query Match
Best Local Similarity 7.2%; Score 140.5; DB 5; Length 363;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLGFKEGTQYTDLTGCGWEYQIQNSAENENNSW-TRVAFAGLKFQDYGSEFDYGR--N 114
:||||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 KIGFKGEDLGNCKAIWOLE---QKASIAGTNSGNGRQSFGLK---GCGTVRAGN 116
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 YGVVY-----DVTSMIDVLEPFQGDYTGSDNFMQORGNFQATYRNDPGL-----VDGL 164
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 LNTVLKDSGDNVAM-----ESGNT-----EDVLGLGTIGRESR 152
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 165 NFAVOYQKNGNPSGEGFTSGV-----TNGRDA-----LRONGDVGGSITYDEGFGIG 215
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 153 EISVRD-----SPVFAFGSSVQYVPRDNANDVDKYKHTKSSRSYHAGLKYENAGFGQ 208
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 216 GAISSSK-----RTDAONTAAVINGNDRAETV-----TGILKYDANNIY--LAAQYTOTYN 264
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 YAGSFAKYADLNTDAERVAANTANAHFVKDYQVHRVYAG--YDANDLYVSAGQYEAAKN 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 265 ATRVGSU-GWANKAQNENVAOYQFDGLRPSLAYLOS-KGKNG---RGYDDEDILKYV 319
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 -NEVGSTGKGGKHETQVAAATPAATRFQ-NVTPRVSYAHGFAKAVNGVDANTQYDQVY--- 321
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 320 DVGATYYFNKNMSTYV 335
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 322 -VGADYDFSKRTSALV 336
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: September 25, 2001, 15:54:31  
Job time: 70 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 ; Search time 16.07 Seconds

(without alignments)  
1739.643 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953  
Sequence: 1 MKSKVLALLIPALLAGAAH.....TRDAGINTDVALGLVYQF 367

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR68:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1 MMECPC	outer membrane por
2	1804	92.4	367	2 B85861	outer membrane por
3	1539.5	78.8	378	1 MMEBPC	outer membrane por
4	1537	78.7	363	2 S51104	outer membrane por
5	1512.5	77.4	378	1 A59139	outer membrane por
6	1295	66.3	377	2 D64888	outer membrane por
7	1213.5	62.1	394	2 S34263	outer membrane por
8	1177	60.3	365	1 MMECNC	outer membrane por
9	1174	60.1	365	1 MMEBPC	outer membrane por
10	1142.5	58.5	366	2 E85729	probable outer mem
11	1109	56.8	351	1 MMECPE	outer membrane por
12	1109	56.8	351	2 B85513	outer membrane por
13	1104	56.5	362	1 MMECF	outer membrane por
14	1104	55.6	362	1 B85619	outer membrane por
15	1086	55.6	351	2 S25520	outer membrane por
16	1065.5	54.6	350	2 S25525	outer membrane por
17	1055.5	54.0	350	2 S3606	outer membrane por
18	1027.5	52.6	363	2 S43159	outer membrane por
19	1002	51.3	369	2 S70847	outer membrane por
20	733.5	37.6	355	2 D85740	partial probable o
21	732	37.5	315	2 T46993	hypothetical prote
22	692	35.4	224	2 P85814	probable outer mem
23	600	30.7	171	2 H64960	outer membrane por
24	592	30.3	382	2 G84971	ompF-like porin [l
25	522.5	26.8	123	2 C85740	partial probable o
26	478	24.5	191	2 G85814	probable outer mem
27	388.5	19.9	134	2 B64961	outer membrane por
28	310	15.9	96	2 C64900	outer membrane por
29	279	14.3	350	2 A82299	outer membrane pro

30	254	13.0	331	2 E82389	probable outer mem
31	215.5	11.0	97	2 A57983	outer membrane por
32	194.5	10.0	371	2 S68072	major outer membra
33	194.5	10.0	371	2 S68069	major outer membra
34	176	9.0	386	2 S68062	major outer membra
35	174.5	8.9	326	2 JN0792	porin-like protein
36	173.5	8.9	385	2 S68066	major outer membra
37	172.5	8.8	385	2 S68067	major outer membra
38	169.5	8.7	385	2 S68070	major outer membra
39	169	8.7	502	2 T46990	hypothetical prote
40	168.5	8.6	361	2 JC6314	major porin protei
41	165	8.4	330	2 PC4425	lectin-like adhesi
42	164.5	8.4	361	2 A30542	major outer membra
43	163.5	8.4	359	2 D64050	major outer membra
44	156.5	8.0	368	2 A82148	probable porin VC1
45	155	7.9	360	2 S17456	outer membrane pro

#### ALIGNMENTS

RESULT 1  
MMECPC  
outer membrane porin ompC precursor - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999  
C:Accession: A20867; A18885; B25029; E64991  
R:Mizuno, T.; Chou, M.Y.; Inouye, M.  
J. Biol. Chem. 258, 6932-6940, 1983  
A:Title: A comparative study on the genes for three porins of the Escherichia coli ou  
A:Reference number: A20867; MUID:83213433  
A:Accession: A20867  
A:Molecule type: DNA  
A:Residues: 1-367 <MIZ>  
A:Cross-references: GB:K00541; GB:M10314; GB:M14188; NID:g147007; PIDN:AAA24243.1; PI  
R:Mizuno, T.; Chou, M.Y.; Inouye, M.  
FEBS Lett. 151, 159-164, 1983  
A:Title: DNA sequence of the promoter region of the ompC gene and the amino acid sequ  
A:Reference number: A18885; MUID:83132326  
A:Accession: A18885  
A:Molecule type: DNA  
A:Residues: 1-40 <MIZ>  
R:Nogami, T.; Mizuno, T.; Mizushima, S.  
J. Bacteriol. 164, 797-801, 1985  
A:Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous r  
A:Reference number: A91809; MUID:86033642  
A:Accession: B25029  
A:Molecule type: DNA  
A:Residues: 32-57 <NOG>  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
A.: Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: E64991  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-367 <BLAT>  
A:Cross-references: GB:AE000310; GB:U00096; NID:g2367131; PIDN:AACT5275.1; PID:g17885  
C:Genetics:  
A:Gene: ompC  
A:Map position: 47 min  
C:Function:  
A:Description: one of the E. coli major outer membrane proteins that form passive dif  
C:Superfamily: outer membrane protein phoF  
C:Keywords: membrane protein; porin; trimer  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-367/Product: outer membrane porin ompC #status predicted <Mat>

Query Match 98.0%; Score 1914; DB 1; Length 367;  
Best Local Similarity 98.1%; Pred. No. 5; 6e-127;

	Matches	360;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	MKSKVLALLIIPALLAAGAAHAEVYNNKDGKNTIDLYGKVDGLHYRSDKNVDGDDTYMRFG	60							
Db	1	MKVYSLSLVLPALLVAGANAHAEEVYNNKDGKNTIDLYGKVDGLHYRSDKNVDGDDTYMRFG	60							
QY	61	FGGEFQVTDQLGTCGOWEFOJOGNSAENENNSWTVFAFAGLKFDVGSFDDYGRNCGVYD	120							
Db	61	FGGEFQVTDQLGTCGOWEFOJOGNSAENENNSWTVFAFAGLKFDVGSFDDYGRNCGVYD	120							
QY	121	VTSWTDVLPPEFGDPTYGSDNEMQORNGNEGATYRNTDFEGLVDGLNFAVOYOGKNGNPGE	180							
Db	121	VTSWTDVLPPEFGDPTYGSDNEMQORNGNEGATYRNTDFEGLVDGLNFAVOYOGKNGNPGE	180							
QY	181	GFTSGVTNNGRALNQNDGVGSGTIDYDEBFGIGGALSSSKRPDAQNTAAYIGNGDAE	240							
Db	181	GFTSGVTNNGRALNQNDGVGSGTIDYDEBFGIGGALSSSKRPDAQNTAAYIGNGDAE	240							
QY	241	TYTGGIGKTDANNIYLAAYOTOTYNATRVGSLGMANKACNFVAAYOFDFGLRPSLAYLQ	300							
Db	241	TYTGGIGKTDANNIYLAAYOTOTYNATRVGSLGMANKACNFVAAYOFDFGLRPSLAYLQ	300							
QY	301	SKKKNLGRGYDEDEDILKTYVDGATYYFNKNMSTVYDYKINLLDNOQFTRDAGINTDNIVA	360							
Db	301	SKKKNLGRGYDEDEDILKTYVDGATYYFNKNMSTVYDYKINLLDNOQFTRDAGINTDNIVA	360							
QY	361	LGILVYOF 367								
Db	361	LGILVYOF 367								

RESULT 2  
 outer membrane protein 1b (tbc) [imported] - Escherichia coli (strain O157:H7)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
 C:Accession: B85861  
 R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: B85861  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-367 <STO>  
 A:Cross-references: GB:AE005174; NID:q12516550; PIDN:AA657350.1; GSPDB:GN00145; UWGP:234  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: ompC  
 C:Superfamily: outer membrane protein phoc

[illegible]

Qy	241	TTTGGKATDANNITYLAAOYTOFNATRVGSLGMARKAONFEVAAYQDFGLRPSLAVIQ	300
Db	237	TTTTGGATKDANNITYLAAOYTOFNATRVGSLGMARKAONFEVAAYQDFGLRPSLAVIQ	296
Qy	301	SKGKNL----GRGYDDEDLIKYVDGATYYFNKNKSTVVDYKINLLDNOFTRDAGINTD	356
Db	297	SKGKNLGYINGNNYDDEDLIKYVDGATYYFNKNKSTVDYKINLLDNOFTRDAGINTD	356
Qy	357	NIVALGLVYQF 367	
Db	357	NIVALGLVYQF 367	

RESULT 3  
KMEBPC  
outer membrane porin ompC precursor - Salmonella typhi  
C:Species: Salmonella typhi  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999  
C:Accession: J00119; S01248; S10122  
R:Punette, J.L.; Alvarez-Scherer, V.; Gosset, G.; Calva, E.  
Gene 83, 197-206, 1989  
A:Title: Comparative analysis of the Salmonella typhi and Escherichia coli ompC genes  
A:Reference number: J00119; MUID:90060831  
A:Molecule type: DNA  
A:Accession: J00119  
A:Residues: 1-378 <PUB>  
A:Cross-references: GB:M1424; NID:g154207; PIDN:AAA27169.1; PID:g154208  
R:Venegas, A.; Gomez, I.; Zaror, I.; Yudelevich, A.  
Nucleic Acids Res. 16, 7721, 1988  
A:Title: The nucleotide sequence of the Salmonella typhi ompC porin gene.  
A:Reference number: S01248; MUID:88319959  
A:Accession: S01248  
A:Molecule type: DNA  
A:Residues: 1-5, 'Q', 7-361, 363-378 <VEN1>  
A:Cross-references: EMBL:X07835; NID:g47796; PIDN:CAA30688.1; PID:g47797  
A:Experimental source: strain Ty2  
R:Venegas, A.  
submitted to the EMBL Data Library, May 1988  
A:Reference number: S10122  
A:Accession: S10122  
A:Molecule type: DNA  
A:Residues: 1-361, 363-378 <VEN2>  
A:Cross-references: EMBL:X07835; NID:g47796; PIDN:CAA30688.1; PID:g47797  
C:Genetics:  
A:Gene: ompC  
A:Map position: 45 min  
C:Superfamily: outer membrane protein phoE  
C:Keywords: membrane protein; porin; trimmer  
F.1-21/Domain: signal sequence #status predicted <SRG>  
F.22-378/Product: outer membrane porin ompC #status predicted <MAT>

[illegible]



[illegible]

## RESULT 4

A:Submitted to the EMBL Data Library May 1994  
A:Description: A porin from *Klebsiella pneumoniae*: sequence homology, three-dimensional  
A:Reference number: S11104  
A:Accession: S11104  
A:Molecule type: DNA  
A:Residues: 1-363 <AB>  
A:Cross-references: EMBL:Z33506; NTD:g2104843; PIDN:CAA63913.1; PID:g619891  
C:Genetics:  
A:Gene: ompK36  
C:Superfamily: outer membrane protein phoe  
C:Keywords: membrane protein; porin; trimer  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-363/Product: outer membrane porin ompK36 #status predicted <MAT>

Query Match	78.7%;	Score 1537;	DB 2;	Length 363;
Best Local Similarity	78.9%;	Pred. No. 1.5e-100;		

QY	1	MKSRYLALILPALLAAGAAHAEYENKNDGKKLDLYGVDGLHFE	SDNKRVDYDGOQTMYRLG	60
Db	1	MKVYVLSLVPALLVAAANAABEYENKNDGKKLDLYGIDILHFE	SDSKDVKDVGQOTMYRLG	60
QY	61	FKGEQVYVTLDTGGYQGEYVIOGNSAENENN-SWTRAFAGLKE	FOPYGSFEDYGRNRYVY	119
Db	61	VKGETOINDQLTGCGMEYVYQANNTSSSDQAWTRAFAGLKE	FGDAGSFDRYRNRYVY	120
QY	120	DVTSMTDVLPEFGSDTYGSDNFMQQRNCFATYRNTDFEGL	VDGLNFAYVYOGKGNPSS	179
Db	121	DVTSMTDVLPEFGSDTYGSDNFLQSRANGVATRYRNSDFE	GLVDGLNFALDYQKGNVSQ	180
QY	180	EGFYSQYVNNGRDMLRONGGCVGSGSTYYD-YEFGIGGLAIS	SSSKRIDAQNTAAYINGNR	238
Db	181	E---GATNNRGKLLKONGGGFTGVSYYDLFDGISAGFAVANSK	RTPDDQN-QLLLEBGH	235
QY	239	AETVTGLKTYDANNIYLAAYOTYQTYNATRYGSLGWMARK	ACQNEFAVAYOYDFGLRPSLAY	298
Db	236	AETVTGLKTYDANNIYLAOTYQTYNATRYGSLGFAPKAK	QNEFEYAAOYQYDFGLRPSVAY	295
QY	299	LQSKGNLGRGYDDEDLKTYVDGATYEFKNMSTVYDYKINL	LDNQFTRDAGINTDNI	358
Db	296	LQSKGKDL-NGYGDQDILKTYVDGATYEFKNMSTVYDYKINL	LDNFSFTRSGISTDY	354
QY	359	VALGLVYQF	367	
Db	355	VALGLVYQF	363	

## RESULT

outer membrane porin C precursor - *Salmonella typhimurium*  
N:Alternate names: ompC protein  
C:Species: *Salmonella typhimurium*  
C:Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 12-Nov-1999

C:Accession: A59139  
R:Negm, R.S.; Pistole, T.G.  
Can. J. Microbiol. 45, 658-669, 1999  
A:Title: The porin OmpC of *Salmonella typhimurium* mediates adherence to macrophages  
A:Reference number: A59139, M0ID:199457705  
A:Accession: A59139  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-378 <NEG>  
A:Cross-references: GB:AF039309, NID:g2773086, PIDN:AA96675.1; PID:g2773087  
A:Experimental source: strain 14028  
A>Note: submitted to GenBank, December 1997  
C:Genetics:  
A:Gene: ompC  
A:Map position: 49.3 minutes  
C:Complex: homotrimer  
C:Superfamily: outer membrane protein phoE  
C:Keywords: homotrimer; membrane protein; porin  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-378/Product: outer membrane porin ompC #status predicted <Mat>

## Query Match

Query Match	Score	DB 1;	Length
Best Local Similarity	77.4%;	1512.5;	378;
	76.6%;	Pred. No. 8e-99;	

Matches	Conservative	Mismatches	Indels	Gaps
294;	26;	41;	23;	6

```

QY      1 MKVYVLLPALLPALLAAGAAHAEYNNKDNKKLDYGVVDGLHFEPSDKDVDSQOTYMRIG 60
Db      1 MKVAVSLVLPALLVAGCAANAEIYNNKDNKKLDLFGVVDGLNFFSDDKSGDGQOTYMRIG 60
QY      61 FKGETOYVDQLTGYGOWEYQIOGNSAENENNSWTRVAFAGLKPODYGSPDYGRNRYGVVD 120
Db      61 FKGETOYVDQLTGYGOWEYQIOGNSQTEGSDSWTRVAFALKKPADAGSPDYGRNRYGVVD 120
QY      121 VTSWTDVLPFEGGDTYGSDFNEMOGRNFATYRNTDFEGLVDGLNPAVQYQGNKNGPSGE 180
Db      121 VTSWTDVLPFEGGDTYCADNEMOGRNGVATYRNTDFEGLVDGLDFALQYQGNKNGSVSGE 180
QY      181 GFETSGVYNNNGDALARONGDDGVGSITDY-EGEFIGAIISSKRT-DAQWT-AAVYING 236
Db      181 -----NTNGSSLNNGMDGDIIGSSLLTAAIEBGFSVGAITTSKRITADQDWTANARLYGNG 234
QY      237 DRAETVYTGGLKYDDANNIYVLAAYVQTYNATRVG-----SLGWANKAKQNEEAAVQYQ 287
Db      235 DRAVYVYTGGLKYDDANNIYVAAYVQTYNATRVFGTSGNSNPTSVGFANKAKQNEEVAAYQY 294
QY      288 FDFEGLRPSLAYLQSKGNKNLGCG----YDDEDILKYVDVGAITYFPNKNMSTYYDYKLTNLD 343
Db      295 FDFEGLRPSVAYLQSKGKDISNGYASGADQDLYKYVDVGAITYFPNNMSTYYDYKLTNLD 354
QY      344 DNOFTROAGINTDNVIALGLVYQF 367
Db      355 KYEFTROAGINTDNVIALGLVYQF 378

```

## 6 RESULT

outer membran porin bl377 precursor - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 20-Aug-1999  
C:Accession: D64868  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
-A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: D64868  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-377 (BLAT)  
A:Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAQ74459.1; PID:g17876666  
A:Experimental source: strain K-12, substrain MO1655  
C:Superfamily: outer membrane protein phob

C/Keywords: membrane protein; porin; trimer  
F.1-21/Domain: signal sequence #status predicted <SIG>  
F.22-377/Product: probable outer membrane porin b1377 #status predicted <OPP>

Query Match	66.3%;	Score 1295;	DB 2;	Length 377;
Best Local Similarity	67.8%;	Pred. NO. 1.4e-83;		
Matches 261;	Conservative 37;	Mismatches 61;	Indels 26;	Gaps 10

QY	1	MKSRYLALLIPALLAAGAAHAAEYVYNNKDGKMLDLYGVADGHLHFEISDKMDVDGDTYRLG	60
Db	1	MKSRYLALLIPALLAAGAAHAAEYVYNNKDGKMLDLYGVADGHLHFEISDKMDVDGDTYRLG	60
QY	61	EKGETQYVLDLTLYGOWEYTOYQGSAAE-NEHNSMTIRAFAGLKKQDYGSFDCYGNICYVY	119
Db	61	EKGETQYVLDLTLYGOWEYVNIQANNHTSKKQSTRIAFAGLKKADYGSFDCYGNICYVY	120
QY	120	DVYSMTDVLPEFGGDTY-GSDNFNQOQKGNFCATYRNTDFGLVDGLNFAVOYQKKNQPS	178
Db	121	DIECTMDLPEFGGDSYTNADNFMTGRANGAVATYRNTDFGLVGNLMAVOYQGN--	176
QY	179	GEGTISCV--NNNRDMLRQNGDVGSGSIYTDY-EGGIGIGALSSKRTDAQ--NTAYI	233
Db	177	EGSGNGGEGNNNRDVRHENGDSGWSITTYDILGMSGAGAAATYSSORTDQVNHNTAA--	233
QY	234	GNQDRAETTYGGGLKYDANNIYLLAAYQTYTNATRFVGSIGW--ANKAONFEAVAYOYQDFG	293
Db	234	GGGRKADAMTGLKYDANNIYLLATMYSETRNMPFEGGSDVAVANKTQNFVETAYOYQDFG	292
QY	292	LRLSLATLYQSGKML-----GRGVDDDLIKYVVNGATYVFNKMSYVYVYKIKILLD	343
Db	293	LRLPVSFELMSKGRDLHAAGADNPAGVDDDLQVATIDIGATYVFNKMSYVYVYDKIKILLD	352

```

RESULT      7
S34263
outer membrane porin ompF precursor - Salmonella typhi
C:Species: Salmonella typhi
C:Date: 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change 20-Aug-1999
C:Accession: S34263
R:Fernandez-Mora, M.; Calva, E.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34263
A:Accession: S34263
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-394 <PER>
A:Cross-references: EMBL:X73237; NID:g602362; PIDN:CAAS1710.1; PID:g311957
C:Genetics:
A:Gene: ompF1
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F,1,21/Domain: signal sequence #status predicted <SIG>
F,22-394/Product: outer membrane porin ompF1 #status predicted <MAR>

```

[illegible]

```

Db      121 D IEAATDIALPEFGGDTYTQTDFVYMLGRTNQVATRYRNDFEGLVEGLFALFOYOGNNEN -G 179
Oy      179 GEGFTSGATNNG -RDALRONDGDGGSLTYDYE -GPGIGAGISSKRRTDNONAAV ---- 232
Db      180 GAGAGEGTCNGNGNKKLARENDGEGMSTDFDEGCLSLGAAYSSDSRSDNQVARGTDCM 239
Oy      233 -----IGNDBAETTYTGGCLTANNITLYLAOYTQTYNATRV -----GSLGMKANQNF 281
Db      240 NERNNYAGGETAEMTIGAKDAYNAVLYLAAMYETRRMNTYYGGNGEGNSISANKTQNF 299
Oy      282 AVAOYQDFEGRLPSLAIYQSKNGKML-----RG-----YDDSDILKYVGVATYYFNKNMST 333
Db      300 VVAOYQDFEGRLPSLAIYQSKNGKMLGGQEVHNRGMWRTDKDLYKYVDGYMTYYFENKNMST 359
Oy      334 YVDKRLINLD -DNOFTRDAGINTDNYALGLYQF 367
Db      360 YVDKRLINLDEDDFYANNNGIATDIDYGVGLYQF 394

```

```

RESULT      8
MMECNC
outer membrane porin pmc precursor - Escherichia coli cryptic lambdaoid prophage DLP1
C:Species: Escherichia coli
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: A25647; S66594; G64787
R:Blasband, A.J.; Marcotte Jr., W.R.; Schnaltman, C.A.
J. Biol. Struct. 261, 12723-12732, 1986
A>Title: Structure of the lc and pmc outer membrane porin protein genes of lambdaoid
A:Reference number: A25647; MUID:86304457
A:Contents: mutant strain CS384
A:Accession: A25647
A:Molecule type: DNA
A:Residues: 1-365 <BLA>
R:Mandl, A.A.; Sharples, G.J.; Mandal, T.N.; Lloyd, R.G.
J. Mol. Biol. 257, 561-573, 1996
A>Title: Holliday junction resolvases encoded by homologous rusa genes in Escherichia
A:Reference number: S66579; MUID:96196428
A:Accession: S66594
A:Molecule type: DNA
A:Residues: 347-365 <MAH>
A:Cross-references: EMBL:X92587; NID:g1051136; PIDD:CAA63325.1; PID:g1051145
R:Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Pernu, N.T.; Burland, V.; Riley, M.;
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64787
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: MNIRAYTSFFNNSSKKGLT', 1-325, 'N', '327-347', 'EGANKSLI' <BLAT>
A:Cross-references: GB:HE000160; GB:U000096; NID:g1186751; PIDD:AMC73634.1; PID:g1186751
A:Experimental source: strain K-12, substrain MG1655
C:Comment: In wild-type strains of E. coli K-12, the pmc open reading frame is inter
ain CS348, the IS5 element has been deleted and pmc is expressed.
C:Genetics:
A:Gene: pmc
A:Map position: 12 min
A:Genome: cryptic lambdaoid prophage DLP12
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F:1-23/Domains: signal sequence #status predicted <SIG>
F:24-365/Product: outer membrane porin pmc #status predicted <MAT>

```

Query Match Similarity 60.3% Score 1177; DB 1; Length 365;  
 Best Local Similarity 62.1% Pred. No. 2,5e-75;  
 Matches 224; Conservative 41; Mismatches 80; Indels 22; Gaps 6

Db 290 GLRPSVAVILQSKGKDLG-VWGDDDLVKRYVDGATFYENKNMSTFVDYKINLLDKNDPTKA 348  
QY 351 AGINTDNIVAGLYTQQF 367  
I::I::I::I::I::I::  
Db 349 LGVSTDIDIVAGLYTQF 365

RESULT 10  
E85729  
probable outer membrane porin protein Z2239 [imported] - Escherichia coli (strain O157:H7)  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
C:Accession: E85729  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanita, E.; Potamoukis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference numbers: AB8480; MUID:21074935; PMID:11206551  
A:Accession: E85729  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-366 <SNO>  
A:Cross-references: GB:AE005174; NID:g12515212; PIDD:AA656297.1; GSPDB:GN00145; UMGP:

[illegible][illegible]



A:Molecule type: protein  
 A:Residues: 23-87, 'E', 89-138, 'G', 140-283, 'L', 285-362 <CHE>  
 R:Nozumi, T.; Mizuno, T.; Mizushima, S.  
 J. Bacteriol. 164, 797-801, 1985  
 A>Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous recombination  
 A:Reference number: A91809; MUID:86033642  
 A:Accession: A25029  
 A:Molecule type: DNA  
 A:Residues: 33-63 <NUG>  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A>Title: The complete genome sequence of *Escherichia coli* K-12.  
 A:Reference number: A64720; MUID:97426617  
 A:Accession: H64832  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-362 <BLAT>  
 A:Cross-references: GB:AE000195; GB:U00096; NID:91787156; PIDN:AMC74015.1; PID:91787160;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ompF; tolF; cmfB; coa; cry  
 A:Map position: 21 min  
 C:Complex: homotrimer  
 C:Function: <POK>  
 A:Description: Forms aqueous channels that facilitate diffusion of small hydrophilic mole  
 C:Function: <REC>  
 A:Description: receptor for bacteriophage T2  
 C:Superfamily: outer membrane protein phoE  
 C:Keywords: membrane protein; porin; trimer  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-362/Product: outer membrane porin ompF #status experimental <MAT>

Query Match 56.5%; Score 1104; DB 1; Length 362;  
 Best Local Similarity 58.9%; Pred. No. 3.2e-70;  
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

```

1 MRSKVLALLIPALLAAGAAAEVYNNKDKNKLIDLYGKVDGLHYFS-----DNKVDGDOT 55
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
2 MKRNILAVIYVALLVAGTANAAEIVYNNKDKNKLIDLYGKVDGLHYFSKNGENSYGNGDMT 61
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
56 YARLGFKEGTQYTDLTGIGOWEYQIQNSAEN---ENNSWTRVAFAGLKFDVGSFDTG 112
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
62 YARLGFKEGTQINSDLTGIGOWEYNNFQNNSEGADQTKNTRLAFAAGLKVDVGSFDTG 121
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
113 RNVGVYDYDTSMVDLPREGSDPTGSDNFMQGRNGATYRNTDFGLVDGLNFAVQYLG 172
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
122 RNVGVYDYDLGTDMLPERGSDPTAVSDDFVGVGVGATYRNSNDFGLVDGLNFAVQYLG 181
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
173 KNGNPSGEGFTSGVTNNGRD-ALRONGDVGSGITVDYEGFGIGAISSSKRTDAQNTAA 231
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
182 K-----NEMDTARNSMGDVGSGISIEYEGFGIVGAYGADRTNLDG-AQ 225
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
232 YVGNDRFAETVYGLKYDANNITYLAQYQTYNATRV-----GSLGANKAONFEAVAY 286
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
226 PLGNGKKAQOMATGKLYDANNITYLAANGETRNATPITNKFNTISGFANKTQDVLVLAQY 285
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
287 QFDGFLRPSLATVLOSCKNLGCGYDEDDILKYVDVATYFKNMSTYVDYKINLLD-DN 345
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
286 QFDGFLRPSLATVTKSKAKV-BEIGVDLVNFEVGATYFKNMSTYVDYKINLLDSDN 344
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
346 QFTPADGINTDNIVALGLVYQF 367
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
345 KL---GVGSDPTAVAGIYQF 362
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||

```

RESULT 14  
 B85619  
 outer membrane protein 1a (Ia,b,F) [imported] - *Escherichia coli* (strain O157:H7)  
 C:Species: *Escherichia coli*  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
 C:Accession: B85619

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanata, E.; Potamousis, K.; Apoda  
 Nature 409, 529-533, 2001  
 A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A:Reference number: A65480; MUID:21074935; PMID:11206551  
 A:Accession: B85619  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-362 <STO>  
 A:Cross-references: GB:AE005174; NID:912514104; PIDN:AA655414.1; GSPDB:GN00145; UMGF:  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: ompF  
 C:Superfamily: outer membrane protein phoE

Query Match 56.5%; Score 1104; DB 2; Length 362;  
 Best Local Similarity 58.9%; Pred. No. 3.2e-70;  
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

```

1 MRSKVLALLIPALLAAGAAAEVYNNKDKNKLIDLYGKVDGLHYFS-----DNKVDGDOT 55
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
2 MKRNILAVIYVALLVAGTANAAEIVYNNKDKNKLIDLYGKVDGLHYFSKNGENSYGNGDMT 61
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
56 YARLGFKEGTQYTDLTGIGOWEYQIQNSAEN---ENNSWTRVAFAGLKFDVGSFDTG 112
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
62 YARLGFKEGTQINSDLTGIGOWEYNNFQNNSEGADQTKNTRLAFAAGLKVDVGSFDTG 121
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
113 RNVGVYDYDTSMVDLPREGSDPTGSDNFMQGRNGATYRNTDFGLVDGLNFAVQYLG 172
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
122 RNVGVYDYDLGTDMLPERGSDPTAVSDDFVGVGVGATYRNSNDFGLVDGLNFAVQYLG 181
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
173 KNGNPSGEGFTSGVTNNGRD-ALRONGDVGSGITVDYEGFGIGAISSSKRTDAQNTAA 231
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
182 K-----NEMDTARNSMGDVGSGISIEYEGFGIVGAYGADRTNLDG-AQ 225
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
232 YVGNDRFAETVYGLKYDANNITYLAQYQTYNATRVGS-----LGANKAONFEAVAY 286
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
226 PLGNGKKAQOMATGKLYDANNITYLAANGETRNATPITNKFNTISGFANKTQDVLVLAQY 285
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
287 QFDGFLRPSLATVLOSCKNLGCGYDEDDILKYVDVATYFKNMSTYVDYKINLLD-DN 345
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
286 QFDGFLRPSLATVTKSKAKV-BEIGVDLVNFEVGATYFKNMSTYVDYKINLLDSDN 344
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
346 QFTPADGINTDNIVALGLVYQF 367
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||
345 KL---GVGSDPTAVAGIYQF 362
  || :|||:||||| || :|||:|||||:||||| ||||| :| :|||

```

RESULT 15  
 S25520  
 outer membrane porin phoE precursor - *Citrobacter freundii*  
 C:Species: *Citrobacter freundii*  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Aug-1999  
 C:Accession: S25520  
 R:Spietings, G.; Ockhuysen, C.; Hofstra, H.; Tommassen, J.  
 submitted to the EMBL Data Library, August 1992  
 A:Reference number: S25520  
 A:Accession: S25520  
 A:Molecule type: DNA  
 A:Residues: 1-351 <SP1>  
 A:Cross-references: EMBL:X68021; NID:940474; PIDN:CAA48162.1; PID:940475  
 A>Note: This is one of the proteins induced when the *E. coli* cells are grown under ph  
 d compounds, and some other negatively charged solutes  
 C:Genetics:  
 A:Gene: phoE  
 C:Complex: homotrimer  
 C:Function:  
 A:Description: allows passive diffusion of small hydrophilic molecules with molecular  
 A>Note: induced under phosphate limitation  
 C:Superfamily: outer membrane protein phoE  
 C:Keywords: homotrimer; membrane protein; porin  
 F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-351/Product: outer membrane porin phoE #status predicted <Opp>

Query Match . 55.6%; Score 1086; DB 2; Length 351;

Best Local Similarity 57.3%; Pred. No. 5.6e-69;

Matches 213; Conservative 58; Mismatches 75; Indels 26; Gaps 9;

```
QY 1 MKSKVLALLPALLAAGAAHAAEYNNKDKNLIDYGRVDGLHYFSDNKKDVGDDQTYMRLG 60
  |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MKKSTLALVVGITASASVQAAEYNNKNGKNKLDYGVKAMHYMTDSDSKDGDSYIRLG 60
QY 61 FKGETQYTDLTGIGOMEYIOGNSAENENNSW-TRVAFGLKFDYGVSPDYGRNIGVY 119
  |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 FKGETQINDELTYGRWEAEFAGNKAESDSNOQKTRLAFAGSKLKNLGSFDYGRNLGALY 120
QY 120 DVTSMTDVLPFEGGDFYTG-SDNFMQORGNFGATYRNTDFGLVDGLNFAYOYOGKNGNPS 178
  |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 121 DVEAWTDMFPEFGGDSQAQTDNFMTRKASGLATYRNTDFGVVDGLDLTLQYQK----- 175
QY 179 GEGFTSGVTNNGDALRQNGDVGSGITYDYG- -FGIGGAISSKRTDAQNTAAYIGNG 236
  |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 176 -----NQDRDYKKQNGDGFSTVYDFGGSDFAVSGATYNSDRTNQNLQTR-GTG 225
QY 237 DRAETTYTGCLKYDANNITYLAQYTYQYMATRVGSLGANKAQNFEAVAYQDFDGLRPSL 296
  |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 226 DKAEMATGKLYDANDIYIATFYSETRNMTPI-SGGEFANKTONFEAVVQYQDFDEGLRPSL 284
QY 297 AYLOSQKKNLGRGYDDEDILKYVDGATYFENKNSYVDYKINLID-DNQFTRDAGINT 355
  |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 285 GYVLSKQKDI-EGVGNEDLVNIDVGATYFENKNSAFVDYKINQLDSDNKL-----GINN 339
QY 356 DNIVAGLVYQF 367
  |||:::|:::|:::|
Db 340 DDIVAGMYYQF 351
```

Search completed: September 25, 2001, 15:54:13  
Job time: 52 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 ; Search time 13.11 Seconds

(without alignments)  
958.945 Million cell updates/sec

Title: us-09-575-061-1

Perfect score: 1953

Sequence: 1 MKSKVALLIPALLAGAAH.....TRDAGITFDNIVALGLVYQF 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1	OMP_C_ECOLI
2	1539.5	78.8	378	1	OMP_C_SALTI
3	1537	78.7	363	1	OMP_C_KLEPN
4	1512.5	77.4	378	1	OMP_C_SALTY
5	1296	66.4	383	1	OMS2_SALTY
6	1295	65.3	377	1	OMP_N_ECOLI
7	1283.5	65.7	376	1	OMP_C_SERNA
8	1241	63.5	374	1	OMP_C_SERNA
9	1220	62.5	342	1	OMP_C_RAHMO
10	1213.5	62.1	394	1	OMS1_SALTY
11	1187	60.8	397	1	YEDS_ECOLI
12	1177	60.3	365	1	NMPC_ECOLI
13	1169	59.9	355	1	POR1_BPPA2
14	1129.5	57.8	350	1	PHOE_ENTCI
15	1109	56.8	351	1	PHOE_ECOLI
16	1104	56.5	362	1	OMP_F_ECOLI
17	1086	55.6	351	1	PHOE_CITFR
18	1065.5	54.6	350	1	PHOE_SALTY
19	1060	54.3	349	1	PHOE_KLEOX
20	1059	54.2	351	1	PHOE_KLEPN
21	1055.5	54.0	350	1	PHOE_SALTY
22	1029.5	52.7	363	1	OMP_F_SALTY
23	1027.5	52.6	363	1	OMP_F_SALTY
24	1002	51.3	369	1	OMP_F_XENNE
25	882	45.2	282	1	OMP_C_SALTY
26	592	30.3	382	1	PORL_BUCAI
27	289	14.8	341	1	OMP_L_PHOPE
28	279	14.3	341	1	OMP_U_VIBCH
29	196	10.0	363	1	OM2B_HAEIN
30	194.5	10.0	367	1	OM2A_HAEIN
31	194.5	10.0	371	1	OM25_HAEIN
32	192.5	9.9	361	1	OM29_HAEIN
33	191.5	9.8	369	1	OM27_HAEIN

34	189	9.7	360	1	OM26_HAEIN	O48216 haemophilus
35	187.5	9.6	353	1	OM28_HAEIN	O48221 haemophilus
36	176	9.0	386	1	OM24_HAEIN	P46026 haemophilus
37	174.5	8.9	326	1	OMP_H_PHOPE	P29739 photobacter
38	173.5	8.9	385	1	OM23_HAEIN	P46025 haemophilus
39	164.5	8.4	361	1	OM22_HAEIN	P20149 haemophilus
40	163.5	8.4	359	1	OM21_HAEIN	P43839 haemophilus
41	154	7.9	348	1	OM22_NEIGO	P20148 neisseria g
42	153	7.8	348	1	OM21_NEIGO	P18195 neisseria g
43	152.5	7.8	385	1	OMP_BORPE	O04064 bordetella
44	141	7.2	351	1	OM32_COMAC	P24305 comamonas a
45	140	7.2	393	1	OM21_NEIMC	P13415 neisseria m

#### ALIGNMENTS

RESULT 1  
OMP\_C\_ECOLI  
ID OMP\_C\_ECOLI STANDARD: PRT; 367 AA.  
AC P06996;  
DT 01-APR-1988 (rel. 07, Created)  
DT 01-APR-1988 (rel. 07, Last sequence update)  
DT 01-OCT-2000 (rel. 40, Last annotation update)  
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMP\_C) (OUTER MEMBRANE  
PROTEIN 1b).  
GN OMP\_C OR MEOA OR PAR.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83213433; PubMed=6304064;  
RA Mizuno T., Chou M.-Y., Inouye M.;  
RT coli outer membrane. DNA sequence of the osmoregulated ompc gene.";  
RL J. Biol. Chem. 258:6932-6940(1983).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12; MG1655;  
RC MEDLINE=97426617; PubMed=9278503;  
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12;  
RC MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,  
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,  
RA Takada J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [4]  
RP SEQUENCE OF 218-367 FROM N.A.  
RX STRAIN=K12 / BHB2600;  
RC Richterich P., Lahey N., Gryan G., Jaehn L., Mintz L., Robison K.,  
RA Church G.M.;  
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1-22 FROM N.A., AND SEQUENCE OF 22-40.  
RX MEDLINE=83132326; PubMed=6297988;  
RA Mizuno T., Chou M.-Y., Inouye M.;  
RT "DNA sequence of the promoter region of the ompc gene and the amino  
acid sequence of the signal peptide of pro-ompc protein of

```

Db 61 FGGEGVQVTDQLTGYGQWMEQIOGNSAENENNSWTRFAFGKLFQVDYGSFDYGNAGVYVD 120
QY 121 VTSWTDVLPFEFGDITGGSDNFMQORGNFGATYTRNTDFEFLVDGLNFVAYIOGKNGPSE 180
Db 121 VTSWTDVLPFEFGDITGGSDNFMQORNGFATYRNTDFEFLVDGLNFVAYIOGKNGPSE 180
QY 181 GTSGTANNGRALNQNGVGSGSTIYDEEGGIGCAISSKRTDQNTAAATGNGDRÆ 240
Db 181 GTSGTANNGRALNQNGDVGSGSTIYDEEGGIGCAISSKRTDQNTAAATGNGDRÆ 240
QY 241 TYTGKLTADANNIYLAAYQTQYTNATRVGSLGWMANKQNEAVAYQYDFGLRPSLAYIQ 300
Db 241 TYTGKLTADANNIYLAAYQTQYTNATRVGSLGWMANKQNEAVAYQYDFGLRPSLAYIQ 300
QY 301 SKGRNLGRCYDDEDILTKYVDGATYTFENKNNSTYYDYKTNLLDDNQFTDAGINTDNIVA 360
Db 301 SKGRNLGRCYDDEDILTKYVDGATYTFENKNNSTYYDYKTNLLDDNQFTDAGINTDNIVA 360
QY 361 IGLVYQF 367
Db 361 IGLVYQF 367

RESULT 2
ID OMPC_SALTI STANDARD: PRT; 378 AA.
AC P09878;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORTIN OMPC).
GN OMPC.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Salmonella.
CX NCBI_TaxID=601;
[1]
RN SEQUENCE FROM N.A.
RA MEDLINE=90060831; PubMed=2684785;
RT Puente J.L., Alvarez-Scherer V., Gosset G., Calva E.;
RT "Comparative analysis of the Salmonella typhi and Escherichia coli
RL ompC genes.";
RL Gene 83:197-206(1989).
[2]
RN SEQUENCE FROM N.A.
RA STRAIN=TY2;
RC MEDLINE=88319959; PubMed=3412902;
RA Venegas A., Gomez I., Zaror I., Yudelevich A.;
RT "The nucleotide sequence of the Salmonella typhi ompC porin gene.";
RL Nucleic Acids Res. 16:7721-7721(1988).
[3]
RN 3D-STRUCTURE MODELING, AND CRYSTALLIZATION.
RA MEDLINE=99332091; PubMed=10405180;
RA Arockiasamy A., Krishnaswamy S.;
RT "Crystallization of the immunodominant outer membrane protein OmpC;
RT the first protein crystals from Salmonella typhi, a human pathogen.";
RL FEBS Lett. 453:380-382(1999).
-1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
-1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.
-1- SIMILARITY: BELONGS TO THE OMPC/POE FAMILY OF PORINS.
-----
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CC -----
EMBL: M31424 AAAA27169.1; -.
EMBL: X07835 CAA30688.1; -.
OR

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AC 052503;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC).
GN OMPC.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_Taxid=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14028;
RA Negm R.S., Pistole T.G.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF039309; AAB96675.1; -.
CC StyGene; SG10675; OMPC.
CC InterPro: IPR001702; -.
CC InterPro: IPR001897; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00182; ECOLIMPORIN.
CC PRINTS: PR00183; ECOLIMPORIN.
CC PROSITE: PS00576; GRAM_NEG_PORIN; 1.
CC Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
CC SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 1 22 378 OUTER MEMBRANE PROTEIN C.
CC SEQUENCE 378 AA; 41299 MW; FC294209A91D79FA CRC64;

Query Match 77.4%; Score 1512.5; DB 1; Length 378;
Best Local Similarity 76.6%; Pred. No. 5.2e-98;
Matches 294; Conservative 26; Mismatches 41; Indels 23; Gaps 6;

QY 1 MKSKVALALIPALLAAGAAHAAEVYKKDKNKLDLYGKVDGLHFSPDNKDYDGDQTYMRIG 60
DB 1 MKKVALSLVLPALLVAGAAHAAEITYNKDKNKLDLFGKVDGLNFSDDKSGDQTYMRIG 60
QY 61 FKGETVDTDLTGYGOMEXYQIOGNSAENENNSWTRVAFAGLKFQDVGSGFDYGRNYYV 120
DB 61 FKGETVNDQLTGYGOMEXYQIOGNOTEGSNDSTWTRVAFAGLKFADGSGFDYGRNYYV 120
QY 121 VTSWTDVLPFEGGDTYGSDNFMQGRNFGATYRNTDFEGLVDGLNFAVQYOGKNGPSE 180
DB 121 VTSWTDVLPFEGGDTYGADNFMQGRNGNATYRNTDFEGLVDGLDQALQYOGKNGSVSE 180
QY 181 GFTSGVTNNGRDLKQNGDVGSGSTYDY-EGFGIGCAISSSKRT-DAONT--AAVIGNG 236
DB 181 -----NTNGRSLNNGDVGSGSTYDYAIGEGFSVGATYTSKRTADQNTANARLYGNG 234
QY 237 DRAETTYGGLKDYDANNIYLAQYTOTYNAATRVG-----SLGNAKAQNEFAVAQYQ 287
DB 235 DRAETTYGGLKDYDANNIYLAQYTOTYNAATRVG-----SLGNAKAQNEFAVAQYQ 294
QY 288 FDEGLRPSLAAYLQSKGKNTLGRG-----YDDEDILKYVDVGYATYFNKMSGYVDYKINL 343
DB 295 FDEGLRPSLAAYLQSKGKNTLGRG-----YDDEDILKYVDVGYATYFNKMSGYVDYKINL 354
QY 344 DNGFTDAGINTDNIVALGLVYQF 367
DB 344 DNGFTDAGINTDNIVALGLVYQF 367

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DB 355 KYEFTDAGINTDNIVALGLVYQF 378

RESULT 5
ID OMS2_SALT1 STANDARD; PRT; 383 AA.
AC 056111;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN S2 PRECURSOR.
GN OMP52.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_Taxid=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JMS-1;
RA Fernandez-Mora M., Calva E.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC -----
CC EMBL: X89756; CA61903.1; -.
CC InterPro: IPR001702; -.
CC InterPro: IPR001897; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00182; ECOLIMPORIN.
CC PRINTS: PR00183; ECOLIMPORIN.
CC Outer membrane; Transmembrane; Porin; Signal.
CC SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 1 22 383 OUTER MEMBRANE PROTEIN S2.
CC SEQUENCE 383 AA; 42183 MW; 47CFB6B5F6A2370F CRC64;

Query Match 66.4%; Score 1296; DB 1; Length 383;
Best Local Similarity 66.8%; Pred. No. 5.3e-83;
Matches 256; Conservative 37; Mismatches 74; Indels 16; Gaps 8;

QY 1 MKSKVALALIPALLAAGAAHAAEVYKKDKNKLDLYGKVDGLHFSPDNKDYDGDQTYMRIG 60
DB 1 MKKVALSLVLPALLAAGAAHAAEITYNKDKNKLDLYGKVDGLHFSPDSSKDDQTYMRIG 60
QY 61 FKGETVDTDLTGYGOMEXYQIOGNSAENEN-NSWTRVAFAGLKFQDVGSGFDYGRNYYV 119
DB 61 FKGETQINDQLTGYGOMEXYQIOGNTGEGSANSWTRVAFAGLKFQDVGSGFDYGRNYYV 120
QY 120 VTSWTDVLPFEGGDTYG-SDNFMQGRNFGATYRNTDFEGLVDGLNFAVQYOGKNGNS 178
DB 120 VTSWTDVLPFEGGDTYG-SDNFMQGRNFGATYRNTDFEGLVDGLNFAVQYOGKNGNS 180
QY 178 GFTSGVTNNGRDLKQNGDVGSGSTYDY-EGFGIGCAISSSKRTDAQ-NNAAYIG 234
DB 178 GFTSGVTNNGRDLKQNGDVGSGSTYDY-EGFGIGCAISSSKRTDAQ-NNAAYIG 234
QY 235 DRAETTYGGLKDYDANNIYLAQYTOTYNAATRVGSL-----GNANKAQNFAVAQYQ 288
DB 241 GDDKADAMTAGLKYDANNIYLAQYTOTYNAATRVGSL-----GNANKAQNFAVAQYQ 300
QY 289 DFLGRPSLAAYLQSKGKNTL--GRGYDDEDILKYVDVGYATYFNKMSGYVDYKINL 345
DB 301 DFLGRPSLAAYLQSKGKNTL--GRGYDDEDILKYVDVGYATYFNKMSGYVDYKINL 360

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QY 346 Q-FTPDAGINTDNIVALGLVYQF 367  
 ID :||||:||||:||||:  
 Db 361 DPFYKADISTDIDVALGMVYQF 383

RESULT 6  
 OMPN\_ECOLI  
 AC OMPN\_ECOLI STANDARD; PRT; 377 AA.  
 P77747; P76854;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN N PRECURSOR (PORIN OMPN).  
 GN OMPN.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97251357; PubMed=9097039;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sampaio K., Takeuchi Y., Wada C., Yamamoto Y., Takeuchi T.;  
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map.";  
 RL DNA Res. 3:363-377(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A., SEQUENCE OF 22-33. AND CHARACTERIZATION.  
 RX MEDLINE=98317278; PubMed=9642192;  
 RA Prilipov A., Phale P.S., Koebnik R., Widmer C., Rosenbusch J.P.;  
 RT "Identification and characterization of two quiescent porin genes,  
 RT ompC and ompN, in Escherichia coli BE.";  
 RL J. Bacteriol. 180:3388-3392(1998).  
 CC -1- FUNCTION: NON-SPECIFIC PORIN.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.  
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 CC -----  
 CC EMBL; AE000234; AAC74459.1; -  
 CC EMBL; D90775; BAA14981.1; -  
 CC EMBL; D90776; BAA14986.1; -  
 CC Ecocore; BG13375; ompN.  
 CC InterPro; IPR001702; -  
 CC InterPro; IPR001897; -  
 CC Pfam; PF00267; Gram-ve\_porins; 1.  
 CC PRINTS; PR00182; ECOLINPORIN.  
 CC PRINTS; PR00183; ECOLIPORIN.  
 CC Outer membrane; Transmembrane; Porin; Signal.  
 FT SIGNAL 1 21

FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.  
 SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;  
 Query Match 66.3%; Score 1295; DB 1; Length 377;  
 Best Local Similarity 67.8%; Pred. No. 6, 1e-83;  
 Matches 261; Conservative 37; Mismatches 61; Indels 26; Gaps 10;

QY 1 MRSKVALLIPALLAAGAAHAAEVYNNKDKLDLYCKVDGLHFEFSNKKDVGQDTYMRIG 60  
 Db 1 MRSKVALLIPALLAAGAAHAAEVYNNKDKLDLYCKVDGLHFEFSNKKDVGQDTYMRIG 60  
 QY 61 FKEGTQVTDQLGYGQWEXQIQNSAE--NENSWTVAFAGLKEQDVSFDYGRNRYVY 119  
 Db 61 FKEGTQINDQLTGYGQWEXYIQANFTSSKNQSWTBLAFAGLKEFADYGSFDYGRNRYVY 120  
 QY 120 DVTSWMDVLPFEGGDTY--GSDNFMQORNGFATRYRTDFGLVDGLNPAVOYGRKNGNS 178  
 Db 121 DIEGWTMDLPFEGGDSYTYNADNFTGRANGVATYRTDFGLVNGINPAVOYQGN-- 176  
 QY 179 GEGFTSGV--TNGRDALRQNGDVGSGITYYDY--EGFGIGATISSKRRDAQ--NTAAVY 233  
 Db 177 -EGASNGQEGTNGRVRHENGSGMGLSTTYDGMGFSAGAATSSDRNDQVNHATA-- 233  
 QY 234 GNGDRAETVYTGKLYDANNIYLAQYTYQYNAVRGSLG--ANKAQNEFAVAQYQDFRG 291  
 Db 234 -GGDKADAWTAGLKVDANNIYLAATMYSETRNMTPEGDSVAIVANKTQNEFVTAQYQDFRG 292  
 QY 292 LRSLSLVLOSCKNL-----GRYDDEDILKYDVATYFENKMSYVDYKINLLD 343  
 Db 293 LRPAVSFLMSKGRDLHAAGADNPAGVDKLVKADIGATYTFENKMSYVDYKINLLD 352  
 QY 344 -DNOFTPDAGINTDNIVALGLVYQF 367  
 Db 353 EDDSFYAANGISTDIDVALGLVYQF 377

RESULT 7  
 OMPN\_SERMA  
 ID OMPN\_SERMA STANDARD; PRT; 376 AA.  
 AC 054471;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPN).  
 GN OMPN.  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-UOC-51;  
 RX MEDLINE=94236242; PubMed=8180703;  
 RA Hutsul J.A.W., Worobec E.A.;  
 RT "Molecular characterization of a 40 kDa OmpC-like porin from Serratia  
 RT marcescens.";  
 RL Microbiology 140:379-387(1994).  
 CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR  
 CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.  
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.  
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 CC -----  
 CC EMBL; L24960; AAA26562.1; -

DR	InterPro: IPR001702; -	
DR	InterPro: IPR001897; -	
DR	pfam: PF00267; Gram-ve_porins; 1.	
DR	PRINTS: PR00182; ECOLNEPORIN.	
DR	PRINTS: PR00183; ECOLIPORIN.	
DR	PROSITE: PS00576; GRAM_NEG_PORIN; 1.	
KW	Outer membrane; Transmembrane; Porin; Phase recognition; Signal	
FT	SIGNAL	1
FT		21
FT	CHAIN	22
FT		376
SO	SEQUENCE	376 AA; 41440 MW; 81227F8351B568E CRC64;
		OUTER MEMBRANE PROTEIN C.

Query Match	65.7%	Score 1283.5	DB 1	Length 376
Best Local Similarity	65.6%	Pred. No. 3.8e-82		
Matches 252	Conservative 48	Mismatches 59	Indels 25	Gaps 8

QY	1	MKSVMALLIIPALLAAGAAHAAEYVYNNKDNKLDLYGKVDGJHYSZDKNDVDDQDQTYRLLG	60
Db	1	MKLAVLSLMPVALLVAGTACAAETLNKNDGKRLDLTGKVDGLHYTSSNNGVGDQDQSYRRFG	60
QY	61	EKGEGQVTDQLTGYGOWEYQIOGNSAENENN-SWTRVAFAGLKEFDQVGSFEDYGRNYSVY	119
Db	61	LRGEQTISDQLTGYGOWEYQANLHHAENODKNKNTTFRYGAFLKFGDYSFEDYGRNTGVLY	120
QY	120	DVYSMTDVLPERGDDTYGSDNFMQORGNFGATTYNTDFFGLGLVDGLNPAVOYQKNGNPSG	179
Db	121	DVAAYTDLPEDFEDMTYGADPFMRQSSGLATYNNDFPGLVDPLNPALOYKNGN-G	178
QY	180	EGATSGVYNNCRDALLRONGDCVGSITFYDEGFCI--GGAISSSKRPDAONTA----AYI	233
Db	179	E-----ETNNCRDVLGONGSGEYGSMSIDM-GYGISAGAFPNRSKRTSEOGANGHONIM	233
QY	234	GNGDRAETTYTGLKYDANNITYLAQYQTYNATPEVGS-----LSGMAKAAONFEAVAOYOF	288
Db	233	GRGGRKAESYSGGLKYDANNIDVYLAFMFYQSYMAAFSGSDSSVYGYAKKAQSFELYYHOF	293
QY	289	DEGLRPSLAYLQSGKGNLGRG-----YDDEDILKYYDVVGATYYFNKNMSTVYDIKINLLD	343
Db	293	DGFLRPFEGVYQOTGKGKDLGRAGNCKDVGDDOLVYKFDVLGATYFENKNMSTVYDIKINLLD	352
QY	344	DNQFTROAGINTDNTVVALGLYOF	367
Db	353	NNDETDAAAGINTDNTVVAAGVLYOF	376

	RESULT	8
CC	OMPF_SERMA	
ID	OMPF_SERMA	STANDARD; PRT; 374 AA.
AC	O33980;	
DT	15-DEC-1998 (Rel. 37, Created)	
DT	15-DEC-1998 (Rel. 37, Last sequence update)	
DT	15-DEC-1998 (Rel. 37, Last annotation update)	
DE	OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).	
GN	OMPF.	
OS	Serratia marcescens.	
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
CC	Serratia.	
OX	NCBI_TaxID=615;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RP	STRAIN-UOC-51;	
RX	MEDLINE=J7419518; PubMed=9274033;	
RA	Hutsui J.A.M., Worddec E.A.;	
RT	"Molecular characterization of the Serratia marcescens Ompf porin,	
RT	and analysis of S. marcescens OmpF and OmpC osmoregulation.";	
RL	Microbiology 143:2797-2806(1997)	
CC	-i- SUBUNIT: HOMOTRIMER (BY SIMILARITY).	
CC	-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.	
CC	-i- SIMILARITY: BELONGS TO THE OMP/C/PHO FAMILY OF PORINS.	
CC	-----	
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DR	EMBL	U81967	AAB69103.1	;	ALT_INIT.
DR	InterPro	IPR001702	;		
DR	InterPro	IPR001897	;		
DR	Pfam	PF00267	Gram-ve_porins	1	
DR	PRINTS	PR00182	ECOLIIPORIN		
DR	PRINTS	PR00183	ECOLIIPORIN		
DR	PROSITE	PS00576	GRAM_NEG_PORIN	1	
KW	Outer membrane; Transmembrane; Porin; Signal.				
FT					
FT	SIGNAL	1	21	POTENTIAL.	
FT	CHAIN	22	374	OUTER MEMBRANE PROTEIN F	
SO	SEQUENCE	374 AA	41184 MW	BB82IDJ385E41049	CRC64

Query Match	63.5%	Score 1241	DB 1	Length	374
Best Local Similarity	64.3%	Pred. No. 3.3e-79			
Matches 249	Conservative 36	Mismatches 68	Indels 34	Gaps	8

[illegible]

RESULT	9
OMP_C_RAHQ	STANDARD; PRT; 342 AA.
ID	OMP_C_RAHQ
AC	033507;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	OUTER MEMBRANE PROTEIN C (PORIN OMP_C) (FRAGMENT).
GN	OMP_C.
OS	Rahmella aquatilis.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC	Rahmella.
OX	NCBI_TaxID=34038;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CF3;
RX	MEDLINE=9812388; PubMed=9473046;
RA	Achouak W., Pages J.M., de Mot R., Molle G., Heulin T.;
RT	A major outer membrane protein of Rahmella aquatilis functions as a
RT	porin and root adhesin.;
RL	J. Bacteriol. 180:909-913(1998).
CC	- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR





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RT Escherichia coli K-12 and phage 82."
RL J. Mol. Biol. 257:561-573(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC MISCELLANEOUS: IN WILD-TYPE STRAINS OF E. COLI K12, THE NMPC OPEN
CC READING FRAME IS INTERRUPTED BY AN ISS INSERTION AND GENERATES A
CC HYBRID OPEN READING FRAME THAT IS NOT EXPRESSED. HOWEVER, IN
CC MUTANT STRAIN CS348, THE ISS ELEMENT HAS BEEN DELETED AND NMPC IS
CC EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M13457; AAA33728.1; ALT_SEQ.
CC EMBL: AE000160; AAC73654.1; ALT_SEQ.
CC EMBL: U82598; AAB40749.1; ALT_SEQ.
CC EMBL: Z35442; CAA84594.1; -.
CC EMBL: X93587; CAA63325.1; -.
CC PIR: A25647; MMECNC.
CC HSSP: P02931; IGFN.
CC EcoGene: EGI0659; nmPC.
CC InterPro: IPR001702; -.
CC InterPro: IPR001897; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00182; ECOLIPORIN.
CC PRINTS: PS00576; GRAM_NEG_PORIN; 1.
CC PROSITE: PS00576; GRAM_NEG_PORIN; 1.
CC Outer membrane; Transmembrane; Porin; Signal.
CC
CC FT CHAIN 1 23 OUTER MEMBRANE PORIN PROTEIN NMPC.
CC FT CONFLICT 24 326 K -> N (IN REF. 2 AND 3).
CC FT SEQUENCE 365 AA; 40316 MW; 6E5128D4847EB4F8 CRC64;
CC
Query Match 60.3%; Score 1177; DB 1; Length 365;
Best Local Similarity 62.1%; Pred. No. 8.7e-75;
Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;
QY 1 MKSKVLAL--LIPALLAAGAAHAAYVYKDKGNKLDLGVKVDGLHYFSDNKNVDGDDQTYMR 58
DB 1 MKKLTVAISAVAASVLAAMSQAQAEIYNKDSNKLDTLGVNAKHYESNSNADGDDTYAR 60
QY 59 LGRGEGTQVTDLTGYQWETQIOGNSAENENNS--WTRVAFGLKQDVSGEDYGRNYG 116
DB 61 LGRGEGTQINDQLTGFGQWETFEKGNRAESQSSKDKTRLAFGLKFGDGSIDYGRNYG 120
QY 117 VVYDVTSMTDVLPEFGDDTY--GSDNFMQGRNGATYRNTDFGLVGLNFAVQYQKNG 175
DB 121 VAYDIGAMFTDVLPEFGDDTYQTQDVFMTQRTATGVAITRRNDFGLVGLNFAVQYQKND 180
QY 176 NPSGEGFTSVTNNGRDALQNDGCVGSGITYDYEGFGIGALISSSKRTDAQNTAAYI-- 233
DB 181 RSPDNTYETG-----NGSGFGFSATYEEGFGIGATYAKSDRPTQYVAGKVL 229
QY 234 ---GNGRAETTYGGGLKYDANNITYLAQTYQTATNATRVGSLGANKRQNEEVAQYQDF 290
DB 230 EVFASGAGNAEVAAGLKYDANNITYLATYSETQNTVFACHFANKRQNEEVAQYQDF 289
QY 291 GLRPSLAYLQSKSKNLGRGVDIEDILKYVDVGAITYYFNKNMSTYVDYKINLLDNDQPTRD 350
DB 290 GLRPSVAYLQSKKRDG--VAGDDQDVKYVDGATYIYFKKMSFTVDYKINLLDKNDPTKA 348
QY 351 AGINTDNIYALGLYQF 367
DB 349 LGVSTDDIVAVGLYQF 365
RESULT 13

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PORT_BPPA2
ID PORT_BPPA2 STANDARD; PRT; 365 AA.
AC P07238;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORIN PROTEIN LC PRECURSOR.
GN LC.
OS Bacteriophage PA-2.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
OX NCBI_TaxID=10738;
RN (1)
RP SEQUENCE FROM N.A.
RA Mashand A.J., Marcotte W.R. Jr., Schaltman C.A.;
RX BBLDLINE=86304457; PubMed=3017988;
RT "Structure of the lc and nmPC outer membrane porin protein genes of
RT lambdaoid bacteriophage."
RL J. Biol. Chem. 261:12723-12732(1986).
CC -1- FUNCTION: PORINS ARE MAJOR PROTEINS FOUND IN THE OUTER MEMBRANES
CC OF GRAM-NEGATIVE BACTERIA WHERE THEY FORM CHANNELS FOR THE
CC NONSPECIFIC PERMEATION OF SMALL SOLUTES (MOLECULES WITH MW LOWER
CC THAN 4000-6000 DALTONS).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: A PORIN GENE CAN ALSO BE FOUND IN THE GENOMES OF
CC CERTAIN LAMBDOID BACTERIOPHAGE, AND ITS PROTEIN IS EXPRESSED IN
CC THE LYSOGENIC STATE. IN E. COLI THE EXPRESSION OF OMPC AND OMPF
CC PROTEINS IS THEN REDUCED SUBSTANTIALLY.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J02580; AAA32301.1; -.
CC PIR: D25647; MMBP2.
CC HSSP: P02931; IGFN.
CC InterPro: IPR001702; -.
CC InterPro: IPR001897; -.
CC Pfam: PF00267; Gram-ve_porins; 1.
CC PRINTS: PR00182; ECOLIPORIN.
CC PRINTS: PR00183; ECOLIPORIN.
CC PROSITE: PS00576; GRAM_NEG_PORIN; 1.
CC Outer membrane; Transmembrane; Porin; Signal.
CC
CC FT CHAIN 1 23 OUTER MEMBRANE PORIN PROTEIN LC.
CC FT CONFLICT 24 365 H -> R (IN AA SEQUENCE).
CC FT SEQUENCE 365 AA; 40290 MW; 0FB0C0531FB9C0205 CRC64;
CC
Query Match 59.9%; Score 1169; DB 1; Length 365;
Best Local Similarity 61.8%; Pred. No. 3.1e-74;
Matches 233; Conservative 41; Mismatches 81; Indels 22; Gaps 6;
QY 1 MKSKVLAL--LIPALLAAGAAHAAYVYKDKGNKLDLGVKVDGLHYFSDNKNVDGDDQTYMR 58
DB 1 MKKLTVAISAVAASVLAAMSQAQAEIYNKDSNKLDTLGVNAKHYESNSNADGDDTYAR 60
QY 59 LGRGEGTQVTDLTGYQWETQIOGNSAENENNS--WTRVAFGLKQDVSGEDYGRNYG 116
DB 61 LGRGEGTQINDQLTGFGQWETFEKGNRAESQSSKDKTRLAFGLKFGDGSIDYGRNYG 120
QY 117 VVYDVTSMTDVLPEFGDDTY--GSDNFMQGRNGATYRNTDFGLVGLNFAVQYQKNG 175
DB 121 VAYDIGAMFTDVLPEFGDDTYQTQDVFMTQRTATGVAITRRNDFGLVGLNFAVQYQKND 180
QY 176 NPSGEGFTSVTNNGRDALQNDGCVGSGITYDYEGFGIGALISSSKRTDAQNTAAYI-- 233
DB 181 RSPDNTYETG-----NGSGFGFSATYEEGFGIGATYAKSDRPTQYVAGKVL 229

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RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE-84297232; PubMed-6089111;  
 RA Deutch A.H., Rushlow K.E., Smith C.J.;  
 RT "Analysis of the Escherichia coli probA locus by DNA and protein  
 sequencing.";  
 RL Nucleic Acids Res. 12:6337-6355(1984).  
 RN [6]  
 RP MUTAGENESIS OF PHE-351.  
 RX MEDLINE-91162638; PubMed-1848301;  
 RA Struyve M., Moons M., Tommassen J.;  
 RT "Carboxy-terminal phenylalanine is essential for the correct assembly  
 of a bacterial outer membrane protein.";  
 RL J. Mol. Biol. 218:141-148(1991).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).  
 RX MEDLINE-91172301; PubMed-1848682;  
 RA Jap B.K., Wallan P.J., Gehring K.;  
 RT "Structural architecture of an outer membrane channel as determined  
 by electron crystallography.";  
 RL Nature 350:167-170(1991).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE-92375189; PubMed-1380671;  
 RA Cowan S.W., Schirmer T., Rummel G., Steiert M., Ghosh R.,  
 RA Paupert R.A., Jansons J.N., Rosenbusch J.P.;  
 RT "Crystal structures explain functional properties of two E. coli  
 porins.";  
 RL Nature 358:727-733(1992).  
 RN [9]  
 RP TOPOLOGY.  
 RX MEDLINE-93172954; PubMed-7679770;  
 RA Struyve M., Visser J., Adriaanse H., Benz R., Tommassen J.;  
 RT "Topology of PhoE porin: the 'eyelet' region.";  
 RL Mol. Microbiol. 7:131-140(1993).  
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN E. COLI CELLS  
 ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS  
 PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,  
 PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED  
 SOLUTES.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC -----  
 CC EMBL: V00316; CA23605.1; -  
 DR EMBL: D83536; BAA7910.1; -  
 DR EMBL: AE000132; AAC73345.1; -  
 DR EMBL: U70214; AAB08661.1; -  
 DR EMBL: X00786; CA23605.1; -  
 DR PIR: A03432; MMECEP.  
 DR PDB: 1PHO; 3I-OCT-93.  
 DR SWISS-2DPAGE: P02932; COLI.  
 DR ECODBASE: B037.O; 6TH EDITION.  
 DR EcoGene: EG10729; phoE.  
 DR InterPro: IPR001702; -  
 DR InterPro: IPR001897; -  
 DR Pfam: PF00267; Gram-ve\_porins; 1.  
 DR PRINTS: PR00182; ECOLIIPORIN.  
 DR PRINTS: PR00183; ECOLIIPORIN.  
 DR PROSITE: PS00576; GRAM\_NEG\_PORIN; 1.  
 KM Outer membrane: Transmembrane; Porin; Signal; 3D-structure.  
 FT SIGNAL 1 21  
 FT CHAIN 22 351  
 FT MUTAGEN 351 351 F->Y,N,S,V: LESS RESISTANT TO TRYPSIN.

FT STRAND 25 26  
 FT STRAND 30 35  
 FT STRAND 37 45  
 FT STRAND 52 53  
 FT STRAND 56 65  
 FT STRAND 71 82  
 FT STRAND 87 88  
 FT STRAND 93 104  
 FT STRAND 105 107  
 FT STRAND 108 116  
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 FT STRAND 124 126  
 FT STRAND 140 141  
 FT STRAND 143 145  
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 FT STRAND 301 313  
 FT STRAND 318 327  
 FT STRAND 334 335  
 FT STRAND 342 350  
 SQ SEQUENCE 351 AA; 38922 MW; 249E2E362C030C9A CRC64;  
 Query Match 56.8%; Score 1109; DB 1; Length 351;  
 Best Local Similarity 58.3%; Pred. No. 4.3e-70;  
 Matches 217; Conservative 53; Mismatches 76; Indels 26; Gaps 9;  
 QY 1 MRSKVALLIPALLAAGAAHAEEVYKDKGKLDYKVDGLHFSDNKKVDGDTYMRIG 60  
 DB 1 MKKSLALVYMGIVASASVQAAEIKYKDKNKLDYKVRAMHYMSDNASKDGQSYIRFG 60  
 QY 61 FKGSTQVTLTGSGWGEYQIOGNSAENEN-NSMTVAFAGLKFQDVGSFDRGRNGVY 119  
 DB 61 FKGSTQVTLTGSGWGEYQIOGNSAENEN-NSMTVAFAGLKFQDVGSFDRGRNGVY 119  
 QY 120 DVTSMVDLPEFGDTYG-SDNFMQGRGNFGATRYNTDFEGLVDGLNFAVOYQKNGNPS 178  
 DB 121 DVEATMDMPERFGDSQAQTDNFMTRKASGLATRYNTDFEGLVDGLNFAVOYQKNGNPS 178  
 QY 179 GEGFTSGVTNNGRDALRQNGDVGSGSITTYDYS-FCIGALISSKRTDAQNTAAIYKNG 236  
 DB 179 -----RDVYKQNGDGGTSLTYDFGSDPAISGAYTNSDRTEQNSR-GTG 225  
 QY 237 DRAETVGLKDYDANNIYLAAYOTRYNATRVGSLGMAKNAQNEFAVAOYQDFGLRPSI 296  
 DB 226 KRAEAMATGLKIDANNIYLAATYSETRKMTPIIG-GFAKNTQNEFAVAOYQDFGLRPSI 284  
 QY 297 AYLOSCKNMLGRGYDEDDILKYVDGATYFNNKMSYVYDKINKLND-DNQETRDAGINT 355  
 DB 285 GYVLSKSKDI-EGIGDEDLVNIDVGATYFNNKMSAFDYKINQDSNKL-----NINN 339  
 QY 356 DNIVAGLYQF 367  
 DB 340 DDIVAGMTYQF 351

Search completed: September 25, 2001, 15:55:22  
Job time: 121 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 25, 2001, 15:53:21 ; Search time 24.55 Seconds  
(without alignments)  
1977.839 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953

Sequence: 1 MKSKVLAALLIPALLAAGAAH.....TRDAGINTNIVALGLVYQF 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: sp-archaea:\*  
3: sp-bacteria:\*  
4: sp-fungi:\*  
5: sp-human:\*  
6: sp-invertebrate:\*  
7: sp-mhc:\*  
8: sp-mammal:\*  
9: sp-organelle:\*  
10: sp-phage:\*  
11: sp-plant:\*  
12: sp-rodent:\*  
13: sp-unclassified:\*  
14: sp-vertebrate:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1787.5	91.5	366	2	Q9RH85
2	1709.5	87.5	364	2	Q9K597
3	1534.5	78.6	378	2	Q9K3E6
4	1296	66.4	377	2	Q85030
5	1250.5	64.0	374	2	Q87754
6	1025.5	52.5	363	2	Q9K3E7
7	1018.5	52.2	333	2	Q9RAW3
8	1018.5	52.2	333	2	Q9RAW2
9	1015.5	52.0	333	2	Q9S613
10	1015.5	52.0	360	2	Q9R889
11	1010.5	51.7	333	2	Q9R859
12	1009.5	51.7	359	2	Q87753
13	862.5	44.2	315	2	Q9EXH8
14	732	37.5	315	2	Q9ZC71
15	518.5	26.5	130	2	Q52641
16	314	16.1	351	2	Q9R8A1
17	296	15.2	96	2	P77519
18	296	15.2	111	2	P94857
19	296	15.2	111	2	P94858

20	296	15.2	111	2	P94860	P94860 klebsiella
21	288	14.7	111	2	P94635	P94635 calymmatoba
22	257	13.2	69	2	P76871	P76871 escherichia
23	254	13.0	331	2	Q9KH02	Q9KH02 vibrio chol
24	232.5	11.9	356	2	Q9KH07	Q9KH07 aeromonas h
25	198.5	10.2	357	2	Q01452	Q01452 haemophilus
26	174.5	8.9	357	2	Q46225	Q46225 haemophilus
27	174.5	8.9	365	2	Q06631	Q06631 haemophilus
28	174	8.9	343	2	Q54340	Q54340 pasteurella
29	174	8.9	361	2	Q06824	Q06824 haemophilus
30	173.5	8.9	370	2	Q01451	Q01451 haemophilus
31	173	8.9	360	2	Q06826	Q06826 haemophilus
32	171	8.8	353	2	Q04339	Q04339 pasteurella
33	169	8.7	50	2	Q9ZC72	Q9ZC72 yersinia pe
34	169	8.7	360	2	Q06823	Q06823 haemophilus
35	168.5	8.6	361	2	Q45106	Q45106 burkholderi
36	168.5	8.6	363	2	Q06828	Q06828 haemophilus
37	168.5	8.6	368	2	Q06833	Q06833 haemophilus
38	167.5	8.6	374	2	Q05107	Q05107 ectothiorio
39	167	8.6	328	2	Q54347	Q54347 pasteurella
40	167	8.6	364	2	Q06827	Q06827 haemophilus
41	166	8.5	328	2	Q54349	Q54349 pasteurella
42	165.5	8.5	364	2	Q06832	Q06832 haemophilus
43	165	8.4	330	2	P94743	P94743 elkenella c
44	164	8.4	346	2	Q52699	Q52699 neisseria g
45	163	8.3	348	2	Q08266	Q08266 neisseria g

## ALIGNMENTS

RESULT 1  
Q9RH85 PRELIMINARY: PRT: 366 AA.  
ID Q9RH85;  
AC Q9RH85;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN OMPC.  
GN OMPC.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-0157:H7;  
RA Yu S.L., Syu W.J.;  
RT "Altered outer membrane protein OmPC in hemorrhagic Escherichia coli  
RT 0157:H7.";  
RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE  
CC (BY SIMILARITY).  
CC EMBL; AF057355; AAF21761.1; -.  
DR HSSP; Q48473; IOSM.  
DR InterPro; IPR001702; -.  
DR Pfam; PF00267; Gram-ve.porins; 1.  
DR PRINTS; PR00182; ECOINTEPORIN.  
DR PROSITE; PS00576; GRAM\_NEG\_PORIN; 1.  
KW Outer membrane; Porin; Signal; Transmembrane.  
SQ SEQUENCE 366 AA: 40499 MW: 644EADI652565C00 CRC64;

Query Match 91.5%; Score 1787.5; DB 2; Length 366;  
Best Local Similarity 91.6%; Pred. No. 1.1e-118;  
Matches 340; Conservative 9; Mismatches 13; Indels 9; Gaps 2;

QY 1 MKSKVLAALLIPALLAAGAAHAEVYKNDKNDLGYKVDGLHFFSDNKKVDGQTYMRG 60  
DB 1 MKKVVSLVPLVAGAAHAAEVYKNDKNDLGYKVDGLHFFSDNKKVDGQTYMRG 60  
QY 61 FNGETQVTDQLTGYGWEYQIQGNSAENENNSWTRVAFGLKFDYGVGSPDYGRNIGVYD 120





09K3E7 PRELIMINARY; PRT; 363 AA.  
 ID 09K3E7  
 AC 09K3E7  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN FX PRECURSOR.  
 GN OMPX.  
 OS Salmonella enterica subsp. enterica serovar Minnesota.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 NCBI\_TaxId=70803;  
 OX NCBI\_TaxId=70803;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SE111;  
 RA Zimmermann H., Wassenaar T.M., Laubenthaler-Preusse H., Petry F.,  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y15843; CAB9614.1; -.  
 DR InterPro: IPR001702; -.  
 DR Pfam: PF00267; Gram-ve\_porins; 1.  
 DR PRINTS: PR00182; ECOLNEIPORIN.  
 DR PROSITE: PS00576; GRAM\_NEG\_PORIN; UNKNOWN\_1.  
 DR SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 23 363 OUTER MEMBRANE PROTEIN FX.  
 FT SEQUENCE 363 AA; 40090 MW; F5058DDEA516859 CRC64;  
 SO SEQUENCE

Query Match 52.5%; Score 1025.5; DB 2; Length 363;  
 Best local Similarity 53.2%; Pred. No. 6.5e-65;  
 Matches 201; Conservative 60; Mismatches 90; Indels 27; Gaps 7;

1 MKRKVALLPALLAAGAAHAAYNNKDKKLDYGVDSGLHFPDNDK--VDDQDTYMR 59  
 2 MKRKILAAVPAALAAATANAETYNKDKKLDYGRVHAWTTTGGSKNDQYTAQ 61  
 60 GFGKGTQVTDLTGYGWEYOIOGNSAEN--NNSWTRVAFAGLKQDVGSFPGYRNYGV 117  
 62 GFGKGTQVTDLTGYGWEYRTKADRAEGQNSNLVRLAFAGLKVAEVSIDYGRNYGI 121  
 118 VYVTSYTDVLPFEGGDTYG---SDNPMQQRNGFATYRTDFFGLVDGLENFAVOYQGN 174  
 122 VYVTSYTDVLPFEGGDTYG---SDNPMQQRNGFATYRTDFFGLVDGLENFAVOYQGN 181  
 175 GNPSGEGFTSGVYNNGRDALRONGDVGSGITDYDEFGAIGSSSKPTDQNTAAYIG 234  
 182 -----QDNHSINSQNGDVGITMAEFDGFTAAVSSSKRTINDQDRD--G 226  
 235 NGDRAETTYGKLYDYANNIYLAQYOTYNA-----TRVSLGMANKQNEFAVAQYOFD 289  
 227 NGDRAESMAVAGATYDANNVYLAAYETRMMSIVENTVTOTVEANKTOULEVAQYOFD 286  
 290 FGLRPSLAIYQSGKNGKRGYDDEDLIKYDVQATYFENKMSSTYDYKTNLDDNQFTR 349  
 287 FGLRPSLAIYQSGKNGKRGYDDEDLIKYDVQATYFENKMSSTYDYKTNLDDNQFTR 345  
 350 DAGINTDNIVALGLVYOF 367  
 346 SSTYGVTDVQAAGVITYOF 363

RESULT 7  
 09RAW3 PRELIMINARY; PRT; 333 AA.  
 ID 09RAW3  
 AC 09RAW3  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE PHOSPHATE PORIN (FRAGMENT).  
 GN PHOE.  
 OS Klebsiella pneumoniae (subsp. ozaenae).  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.  
 OX NCBI\_TaxId=574;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=I436;  
 RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Sriprakash K.S.,  
 RT Kemp D.J.;  
 RT "Phylogenetic analysis of Calymmatobacterium granulomatis";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBUNIT. HOMOTRIMER (BY SIMILARITY)  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE  
 (BY SIMILARITY).  
 CC EMBL: AF009229; AAD21517.1; -.  
 DR HSSP: P02932; PHO.  
 DR InterPro: IPR001702; -.  
 DR Pfam: PF00267; Gram-ve\_porins; 1.  
 DR PRINTS: PR00182; ECOLNEIPORIN.  
 DR PROSITE: PS00576; GRAM\_NEG\_PORIN; 1.  
 KW Outer membrane; Porin; Signal; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 333 333  
 FT SEQUENCE 333 AA; 36839 MW; 68AF347207770ABA CRC64;  
 SO SEQUENCE

Query Match 52.2%; Score 1018.5; DB 2; Length 333;  
 Best local Similarity 56.5%; Pred. No. 1.8e-64;  
 Matches 200; Conservative 53; Mismatches 76; Indels 25; Gaps 8;

8 LILPALLAAGAAHAAYNNKDKKLDYGVDSGLHFPDNDKVDYDQDTYMR 67  
 1 LMMGVASATQTAAYNNKANKLDYGVKIKAMHFSYDSDKSDQTYVRFKIGETQI 60  
 68 TDLTGYGWEYOIOGNSAENNSWTRVAFAGLKQDVGSFPGYRNYGVYVTSYMTQY 127  
 1 NDULTYGRWSEFSGKNTESDSQKTRLAFAGVKLNKNGSPFYGNLGLVDEAWTDM 120  
 128 LPEFGDITYG--SDNPMQQRNGFATYRTDFFGLVDGLENFAVOYQGNPSGEGFTSGV 186  
 121 LPEFGDITYG--SDNPMQQRNGFATYRTDFFGLVDGLENFAVOYQGNPSGEGFTSGV 167  
 187 TNGGRALRONGDVGSGSTIYDEG--FGGGAIGSSSKPTDQNTAAYIGNDRAETTYG 244  
 168 -NGRRAKKQNGDVGSTISYDFGSDFAVAAYTSSDRTDQNLAR--GQSKAAMAT 225  
 245 GLKYDANNIYLAQYOTYNAATRVGSLGMANKQNEFAVAQYOFDGLRPSLAIYQSGK 304  
 226 GLKYDANNIYLAQYOTYNAATRVGSLGMANKQNEFAVAQYOFDGLRPSLAIYQSGK 284  
 305 NLGRGYDDEDLIKYDVQATYFENKMSSTYDYKTNLDDNQFTRDAGINTDN 357  
 285 DI-EGVGSDELVNYIDVGLTYNNKNNNAFVDYKINQLKSDNKL---GINDD 333

RESULT 8  
 09RAW2 PRELIMINARY; PRT; 333 AA.  
 ID 09RAW2  
 AC 09RAW2  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE PHOSPHATE PORIN (FRAGMENT).  
 GN PHOE.  
 OS Klebsiella pneumoniae subsp. rhinoscleromatis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Klebsiella.  
 NCBI\_TaxId=39831;  
 OX NCBI\_TaxId=39831;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC5046;  
 RC MEDLINE=20023050; PubMed=1055350;  
 RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Sriprakash K.S.,  
 RT Kemp D.J.;  
 RT "Phylogenetic evidence for reclassification of Calymmatobacterium



```

Db      62 GFGGRTQINTDLTGFQGWEMRTKADRAEGEQNSNLVRLAFAGLKAEVGSIDYGRNYGI 121
      118 YVYVSTWTDVLPREGGDTYG---SDNFMQORGNFAGATRTDPEFGLVDGLNFAVOYQGN 174
      122 VYVESTTDAPYFSGTWTGAVTDNMTSRAGGLLTRYNSDFEGLVDGLSFQYQGN 181
      175 GNSGEGFTSGVYNNGRDALRONGDVGCSITYDEFGFISGGAISSSKRPDAONTAAYIG 234
      182 -----QDNHSINSQNGDDGYGTMAIEFDGFGYTAIYNSKRTINDODRD--G 226
      235 NGDRAETTYGGLKYDANNITLAAQYTOTYNA-----TRVSLGMANKQNEFAVAOYQFD 289
      227 NGRABESWAGAKYDANNVYLAAYIAETRNMSIYENTVTDTEAMANKQMLEVAOYQFD 286
      290 FGLRPLSLAYLOSCKNLRGRIYDEDDILKYVDGATYFNKNMSTYDYKINLDDNQFTR 349
      287 FGLRPLSLAYLOSCKNLRGRIYDEDDILKYVDGATYFNKNMSTYDYKINLDDNQFTR 345
      350 DAGINTDNIVALTGLV 364
      346 SSYVGTDGDAAGVIV 360

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RESULT 11
Q9RR59 PRELIMINARY: PRT: 333 AA.
ID 09RR59
AC 09RR59:
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE PHOSPHATE PORIN (FRAGMENT).
GN PHO.
OS Calymmatobacterium granulomatis
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Calymmatobacterium.
OX NCBI_TaxID=39824;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20023050; PubMed-10555350;
RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Stripakash K.S.,
  Kemp D.J.,
  Phylogenetic evidence for reclassification of Calymmatobacterium
  granulomatis as Klebsiella granulomatis comb. nov.*;
  Int. J. Syst. Bacteriol. 49:1695-1700(1999).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
  (BY SIMILARITY).
DR EMBL: AF009231; AAD21519.1; -.
DR HSSP: P02932; IPHO.
DR InterPro: IPR001702; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Porin; Signal; Transmembrane.
FT NON_TER 1
FT TER 333
SQ SEQUENCE 333 AA; 36786 MW; 7CEA2F68B998BB0A CRC64;

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Query Match 51.7%; Score 1010.5; DB 2; Length 333;  
 Best Local Similarity 56.2%; Pred. No. 6.6e-64;  
 Matches 199; Conservative 53; Mismatches 77; Indels 25; Gaps 8;

```

QY 8 LILPALLAAGAAHAEEVYNNKDKKLDLYGVGLHFFSDNKRVDGDO--TYMRL 67
      1 LMMGVASTATQQAEEVYNNKDKKLDLYGVGLHFFSDNKRVDGDO--TYMRL 60
      68 TQDLTGYQWMEYQIOGNSAENENNSWTRVAFAFLKFDQVSGFYGRNYGVYVTSMTDV 127
      61 NDLTGYQWMEYQIOGNSAENENNSWTRVAFAFLKFDQVSGFYGRNYGVYVTSMTDV 120
      128 LPBEGGDTYG--SDNFMQORGNFAGATRTDPEFGLVDGLNFAVOYQGNPNPSEGTSGV 186

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Db      121 FPEGGSSAQTDNFMTRKASGLATYRNDFEGLVDGLDITLQYQCK----- 167
      187 TNGRDLALRONGGCGVGSITYDEG--FGIGGAISSSKRPDAONTAAYIGNDRAETTYG 244
      168 -NEGCAKQKONGGCGVGSITYDEG--FGIGGAISSSKRPDAONTAAYIGNDRAETTYG 225
      245 GLKYDANNITLAAQYTOTYNAATRVGSLGMANKQNEFAVAOYQFDGFLRPLSLAYLOSCK 304
      226 GLKYDANNITLAAQYTOTYNAATRVGSLGMANKQNEFAVAOYQFDGFLRPLSLAYLOSCK 284
      305 NIGRGVDEDDILKYVDGATYFNKNMSTYDYKINLDDNQFTRDAGINTDN 357
      285 DI-EGVGSIEDLVNYIDVGLTYFNKNMNAFVDYKINQLKSDNKL-----GINDD 333

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RESULT 12
Q87753 PRELIMINARY: PRT: 359 AA.
ID 087753
AC 087753:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE OMPK35 PORIN PRECURSOR.
GN OMPK35.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-KT755;
RA Hernandez-Alles S.;
  Thesis (1998): Universidad de les Illes Balears, Valencia, Spain.
DR EMBL: AJ011501; CA09665.1; -.
DR HSSP: P02931; IGEN.
DR InterPro: IPR001702; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
KW Signal.
FT SIGNAL 1
FT CHAIN 23
FT POTENTIAL.
FT OMPK35 PORIN.
SQ SEQUENCE 359 AA; 39510 MW; 12D518340058E5BB CRC64;

```

Query Match 51.7%; Score 1009.5; DB 2; Length 359;  
 Best Local Similarity 53.5%; Pred. No. 8.6e-64;  
 Matches 200; Conservative 54; Mismatches 97; Indels 23; Gaps 6;

```

QY 1 MKSKVALLIPALLAAGAAHAEEVYNNKDKKLDLYGVGLHFFSDNKRVDGDO--TYMRL 59
      2 MKRNILAVIIPALLVGAANAEEVYNNKDKKLDLYGVGLHFFSDNKRVDGDO--TYMRL 61
      60 GKGFTQVTDVLPREGGDTYG---SDNFMQORGNFAGATRTDPEFGLVDGLNFAVOYQGN 119
      62 GKGFTQVTDVLPREGGDTYG---SDNFMQORGNFAGATRTDPEFGLVDGLNFAVOYQGN 121
      120 DTSWTDVLPREGGDTYG--SDNFMQORGNFAGATRTDPEFGLVDGLNFAVOYQGNNGNS 178
      122 DVEAATDMLVWGGDGMWNTDNYMTGRNGVATYRNDSDFEGLVDGLSFALQYQGN---- 177
      179 GKGFTSGVYNNGRDALRONGDVGCSITYDE--FGIGGAISSSKRPDAONTAAYIGND 237
      178 -----DHRALRKQNGDGEFSTAATYAFNGIALSAGYSSNSRVQKAD---GND 225
      238 RAETTYGGLKYDANNITLAAQYTOTYNAATRVGSLGMANKQNEFAVAOYQFDGFLRPLSLA 297
      226 KAFAWATSAKYDANNITLAAQYTOTYNAATRVGSLGMANKQNEFAVAOYQFDGFLRPLSG 285
      298 YLOSCKNLT-----GREGVDEDDILKYVDGATYFNKNMSTYDYKINLDDNQFTRDAGI 353
      286 YVOTKGDLOSRAFGSGDADLVKTIENGVTWYFNKNMNAFVDYKINQLKSDNKL-----GINDD 345

```





Best Local Similarity 71.5%; Pred. No. 1e-29;  
Matches 93; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

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QY 23 EYNNKDSNKLDELGVKVDGLHYFSDNKKVDGDDQTYMRGLGFKGETQVTDQLTGYGOMEYQIQ 82
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EYNNKDSNKLDELGVKVDGLHYFSDNKSADGDSQSYMRGLGFKGETQINNLTGYGMEYQAS 60
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 83 GNSAENEN-NSWTRVAFAGLKFQDVGSFDYGRNYGVYDVTSWTDVLPFEGDPTGSDNF 141
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LNTGESEDANNFTRVGFAGLKFQDWSLSDYGRNYGVYDVAANTDVLPEFGDPTGADNF 120
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 142 MQQRGNFGAT 151
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 MFORANGVAT 130
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Search completed: September 25, 2001, 15:55:03  
Job time: 102 sec